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AL066286 Drosophil
BX416727 BX416727
BX436369 BX436369
AG127412 Pan trogl
                                                                                                  October 29, 2003, 21:18:11; Search time 2502.29 Seconds (without alignments) 8935.871 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                      22781392 segs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                               OM nucleic - nucleic search, using sw model
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BX416727
BX436369
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AL066784 Drosophil AL287287 Tetraodon AL581589 AL581589 AL531397 AL581877 AQ543305 HS. 51387 B. AL071370 Drosophil CD501049 CD548-F07 AL548181 AL548181 AG133408 Pan trogl BX443342 BX443342 BX385076 BX385076 BX596157 SP_B8007 AL102202 Drosophil AL0686379 Drosophil AL068637 Drosophil AL068607 Drosophil AL068607 Drosophil AL068607 Drosophil AL068607 Drosophil	BX436853 BX736853 AG135357 Pan trog1 B12686 F27J14-T7 I BX418086 BX418086 AG135322 Pan trog1 AG137085 Pan trog1 AG137085 Pan trog1 AG137085 Pan trog1 AG13328 Pan trog1 AG73329 BS 5387 B AG13328 Pan trog1 AG13532 Pan trog1 BZ696114 SP Ba007 AG127518 Pan trog1 BZ696114 SP Ba007 AG13682 Pan trog1 BZ696114 SP Ba007 AG13682 Pan trog1 BZ4990 Pan trog1 AG13682 Pan trog1 AG13683 Pan trog1 AG13683 Pan trog1 AG13683 Pan trog1	DNA linear GSS 03-JUN-1999 Be survey sequence TET3 end of BAC # from Drosophila melanogaster (fruit e. it fly) la; Hexapoda; Insecta; Pterygota; era; Brachycera; Muscomorpha; Drosophila. scope - Centre National de Sequencage: NGE (B-mail: seqref@genoscope.cns.fr scope - Centre National de Sequencage: NGE (B-mail: seqref@genoscope.cns.fr sequence was carried out as part of a sequence was carried out as part of a sequence was carried out as part of a sey brosophila Genome Project (BDGP). ysical map of the Drosophila see BACs. For further information ly. Org The BDGP Drosophila see BACs for further information prepared by Kazutcyo Osoegawa and prepared by Kazutcyo Osoegawa and long's laboratory in the Department of
CNSO073W CNSO4ENY AL531977 AL531977 AL531977 AQ743305 CD501049 AL548181 AG133080 BX443342 BX385076 BX385076 BX385076 CNSO12Z4 CNSO12Z4 CNSO12Z4 CNSO12Z4 CNSO12Z4	BX436853 B12686 BX418086 BX418086 BX13132 AG137085 AG137085 AG137085 AG137080 AG137080 AG13528 AG136010 BX410248 AG127518 AG127518 AG127518 AG127518 AG137990 CNSO11TM CNSO1TM CNSO1TM CNSO1TM CNSO1TM CNSO1TM CNSO1TM CNSO1TM CNSO1TM	895 genoo brary quenc (fru: (fru: Dipplae; J Bae; J Backei 3 a pl Ganos Como Como Como Como Como Como Como Co
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1003 99 99 4 89 99 99 99 99 99 99 99 99 99 99 99 99	4444 6699999999999999999999999999999999	81 Mar
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Homo sapiens (human)
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCOI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 712)

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                                                                                                                                            /organism="Drogophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/note="end : TET3"
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THYMUS Homo sapiens cDNA clone CSOCAP001YM12
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1180)
                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="CSODAGIIYI14"
/tissue type="NBUROBLASTOMA"
/clone_Ib="Howspiens NEUROBLASTOMA"
/clone_Ib="Howspiens NEUROBLASTOMA"
/note="Vector: pcWVsPoRT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned it
the Not I and EcoRV sites of the pcWVsPoRT 6 vector.
Library was not normalized."
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                                                                                  Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Inbrary was constructed by Life Technologies, a division of
Invitrogen. Contact : Ferry Liang Email : fliangelifetech.com Uhttp://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODA011BE07QP1.
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Best Local Similarity 14.1%; Pred. No. 6.1e-09;
Matches 57; Conservative 221; Mismatches 127; Indels
Pull-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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BX436369 Homo sapiens T
5-PRIME, mRNA sequence.
BX436369
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                          17412 946 bp DNA linear GSS 04-NOV-2001 troglodytes DNA, clone: PTB-138E06.R, genomic survey sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 AACAAAACACACCACAAANACACAAGAACAACAAANNAAAAACCCCACACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell type="lymphoblast"
/clone lib="PTB Chimpanzee Male BAC Library"
351 c 31 g 23 t 36 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 374; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 946
/organism="Pan troglodytes"
/nol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-138E06.R"
                                                                                                                                                                                                                                                                                                         Pujjyama,A., Hattori,M., Toyoda,A., T
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                           Pan troglodytes (chimpanzee)
Pan troglodytes
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              612 AAAAAGHYYNTKHHYTYY 595
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed
with a NotL-Oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
154 c 191 g 420 t 288 others
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BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BRail: sequefégenoscope.cns.fr / Fechnologies, a division of
Invitrogen. This sequence belongs to sequence cluster 516.f For
more information about this cluster, see
more information about this cluster, see
cgi-bin/cluster.cgi?seq=CSOCAP001BG06QP1&cluster=516.f. Contact
Feng Liang Email: fliangelifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP001BG06QPF1.
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                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP001YM12"
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 BVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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Genome Res. 10 (7), 939-949 (2000)
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                                                                            DB 29;
                                                                                                .3e-07;
                                                                        11.2%; Score 103.2;
24.8%; Pred. No. 2.3
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Tetraodon nigroviridis
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Submitted (02-UUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Droscophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Droscophila melanogaster genome using these BACs. For further information please see http://www.fruifiy.org The BDGP Droscophila melanogaster BAC library was prepared by Kazutcyo Goegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of broscophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14009 of RPCI-98 library from Drosophila melanogaster (fruit AL066784
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ACCCTGCAGCATATGCAGCAATCCAACCTGCTGGGCTATCTGCAAAAGAATACCAAA
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/clone lib="RPCI-98"
/note="end : TET3"
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                                  Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedax - France
Bmail: sequelogecope.cns.fr who: www.genoscope.cns.fr
was not normalized. Library was constructed by Life Technologies,
division of Invitrogen. This sequence belongs to sequence cluster
division of Invitrogen. This sequence belongs to sequence cluster
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODG004CC08NP1&cluster=8262.f. Contact :
Feng Liang Email : filangalifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODG004CC08NP1.
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Pred. No. 7.2e-07;
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              Contact: Genoscope
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- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                            sequence ID : COBG104DH07LP1~end : T7"
g 409 t 71 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 AAATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACC
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                                                                                                                                                                                                                                                                                                                                                                                        11.1%; Score 101.8; DB 29; Length
46.0%; Pred. No. 3.8e-07;
.ive 36; Mismatches 222; Indels
                                                                                                                                                                  /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="104P14"
/clone lib="G"
/note="Genoscope sequence ID : C0BG1
a 86 c 254 g 409 t 71 c
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/Glone lib-*RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

301 c 16 g 15 t 49 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                            GSS 16-JUL-1999
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                                                                                                                                                       Tel: (206) 616-3818
Fax: (206) 616-3818
Email: jwallace@u.washington.edu
Clonea are derived from the human BAC library RPCI-11. For BAC
Clonea are derived from the contact Pieter de Jong
(pieter@dejong.med.buffalo.edu. Clonea may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1141)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                            806 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
746 CTGCTCACCAACAACACCACAGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                       HS 5387 B2 B02 SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=963 Col=4 Row=D, genomic survey sequence.
                                                                                                                                                                                                                  Gaps
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
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Pred. No. 9.1e-07;
0; Mismatches 425;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=963 Col=4 Row=D"
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Plate: 963 row: D column: 4
Seg primer: SP6
Class: BAC ends
High quality sequence stop: 1141.
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Best Local Similarity 46.3%;
Matches 370; Conservative 0
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/dev_stage=fetal"
/dev_stage=fetal"
/clone_lib="momo sapiens FETAL LIVER"
/clone_lib="momo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT_6; lst strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."

208 c 323 g 416 t 93 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODW003CB02QP1&cluster=8045.f. Contact :
Feng Liang Email : fliangedlifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODW003CB02QP1.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                            Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Brigg 191006 BVRY cedex - France
Bmail: seqretégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8045.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            386 CAACCCACAACAGTCAAGACTAAAAACACAAACAACCCAAAACACAGCAAGCCC
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                                                      AL531977
AL531977 Homo sapiens FETAL LIVER Homo sapiens CDNA clone CSODW003YD03 5-PRIME, mRNA sequence.
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Best Local Similarity 41.7%; Pred. No. 7.7e-07;
Matches 223; Conservative 52; Mismatches 260; Indels 0
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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/clone="CS0DM003YD03"
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/clone lib="RPCI-98"
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                      680 APACRARARARCRACCRACARARARCRCRARARCRCCCCRARARARARARARARARA 739
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                                               ATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGA--TG
                                                                     363 CACCAGGAGTCAAGTCAAACCTGCAACCACAACAGTCAAGACTAAAAAACACAACAA
                                                                                                                                                                                                                                          483 CCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACA
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Web: www.genoscope.cns.fr/
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named REC1-98 and was constructed by partial BCOMI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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1081 AAAMACMMWAMACAAAAMACMWACAMWAMAWAMMWACAGMEHWCWKWMWM 1022
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          598 AACCACCACCAAGCCTACAAAAAACCAACCTTCAAGACAACCAAAAAAGATCTCAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atch 10.8%; Score 99; DB 29; Length 11 sal Similarity 25.6%; Pred. No. 1.1e-06; Indels 104; Conservative 145; Mismatches 157; Indels
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Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanogaster"
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    .1101
    /organism="Drosophila me/mol_type="genomic DNA"
    /db_xref="taxon:7227"
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us-09-462-816-1.rst

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EST 31-MAY-2003
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E 1 (Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished

On Feb 15, 2001 this sequence version replaced gi:12882945.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 sequencepe.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 113.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1034EC102Piccluster=113.r. Contact:
Feng Liang Email: filangaliferech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope Sequence ID: CSOD1034EC10PI.
                                                                                                                                                                                                                                                                                                                                                                     485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL548181 1200 bp mRNA linear EST 31-MAY-2003
AL548181 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CSODI034YE02 5-PRIME, mRNA sequence.
AL548181
                                                                                                                                                                                                                              857
         /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homos sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 362 c 185 g 95 t 111 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1200)
                                                                                                                                       618 AAAAACCAACCTTCAAGACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGG
                                                                                                                                                                                798 CCTTCCACTCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCG
                                                                                           738 CAACTACACTGCTCACCAACACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAA
                                                    9; Length 1200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               858 AGCACCCATCACAACCCTCATCTCCACCCAACACA 895
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Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="CS0DI034YE02"
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TITLE
JOURNAL
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ALS48181
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                                                                                                                                                                                                                                                                       CA 94305-5329, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 CAAACCIGCAACCCACAAAAGICAAGACIAAAAACACAACAACAACCAAACAACCA
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                                                                                                                                                                                                Contact: Kingsley, DM
HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford,
Tel: 650 725 5554
Fax: 650 725 7739
Email: kingsley@cmgm.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Gasterosteus aculeatus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="Salinas river, CA"
/db_xref="taxon:69293"
/clone="CDA48-F07"
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High quality sequence stop: 263.
Location/Qualifiers
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Best Local Similarity 45.77
Matches 319, Conservative
                                                                                                                                                                                  Unpublished
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                                                                                                                                                     TITLE
JOURNAL
COMMENT
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10.5%; Score 96.6; DB 29;
Best Local Similarity 47.3%; Pred. No. 2.6e-06;
Matches 354; Conservative 0; Mismatches 390;
                 R&D process and
                                                                                                                                                                                                                          1..1024
/organism="Pan troglodytes"
/mol type="genomic DNA"
/db xref="taxon:9598"
/clone="PTB-145K08.R"
                                                                                                                                                                                                                                                                                                                                                                                                                              40 t
                                                                                                                                                                                                                                                                                                                                                /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanze
460 c 23 g 44
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                                                                                                                                                                                                      Location/Qualifiers
            was generated during the
                                                                                                                                  : pKS145
                                                                                     Sequencing: M13Rev
                                     clone tracking errors.
                                                                                                                                Vector : pKS1
R.Site 1 : SacI
R.Site 2 : SacI
                                                         PRIMERS
                                                                                                       LIBRARY
                                                                                                                                                                                                                                                                                                                                                                                                                            495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-Chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG133080 1024 bp DNA linear GSS 04-NOV-2001
Pan troglodytes DNA, clone: PTB-145K08.R, genomic survey sequence.
AG133080
                                                                                          CATACAAGATGCAACAAGCCAGATCAAGAACACAACAACCAAACATACCTCAACATCC 291
                                                                                                                                                                                                                                         TCAGCTTGGAATCAGCTTCTCCAATCTGTGAAATTACATCACAAACCACCACCATACT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                   CACAACAACAACCCA----AACACCAAGCAGCAAGCCCACTACAAAACAACGCCAAA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             872
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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          Gaps
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watenabe, H. and Sakaki, Y.
Direct Submission
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BAC end sequences of Library PTB
     82; Mismatches 279; Indels
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Pan troglodytes
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Contact: Genoscope
Genosco
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BX385076 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CSODL006YE12 3-PRIME, mRNA sequence.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the PCMVSPORT 6 vector, Library was normalized."
175 c 126 g 196 t 170 others
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/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                                                                AGAAAACCACCACCAACCTACAAAAAAACCAACCTTCAAGACAACCAAAAAAAGATCTCA
                                                                                                                                                                                        654 AACCTCAAACCACTAAACCAAAGGAAGTACCCACCACCAAGCCCACAGAAGAGCCAACCA
                                                                                                                                                                                                                                                                                                                                                                714 TCAACACCACCAAAACAAACATCACAACTACACTGCTCACCAACAACACCACAGGAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          834 CTICTCAAGTCTCCACAACATCCGAGCACCCATCACAACCCTC 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 CCCCCCCCCCCCCCCCCCCCCCMCMCMCMCACYCCCCCCCMMC 114
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODL006YE12"
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Best Local Similarity 38.93
Matches 167; Conservative
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/db xref="taxon:9606"
/clone="CSOMPHOINFO4"
/tissue_type="T CELLS (JURKAT CELL LINE)"
/clone="Lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/clone="lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and Ecory sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3806.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cS0DH001DC02NP1&cluster=3806.r. Contact;
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invirogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DH001DC02NP1.
                                                                                                                                                                                        EST 15-MAY-2003
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                                                                                                                                                                                     linear EST 15-MAY-200:
LINE) Homo sapiens cDNA
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length, CDNA libraries and normalization
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Best Local Simi:
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BX443342/c
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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351 TAGCTTCAACAACACCAGGAGTCAAGTCAAACCTGCAACCCACAACAGACTAAAA 410
        471 CACCAAACAAACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCA 530
                                                             792 AAAMMACMAAAAAMCCCAWAAAAAMAMMCMCAAAAAAACCCMCAAAAAAACCCCCCAM 851
                                                                                 591 GAAAGAAAACCACCACCAAGCCTACAAAAAAACCAACCTTCAAGACAACCAAAAAAATC 650
                                                                                                                    1092 AAAMCMMCC 1100
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Search completed: October 30, 2003, 01:15:23 Job time: 2507.29 secs

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LENGTH: 15223 base pairs
TYPE: nucleic acid
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US-09-847-173-1
376.6
4.4.7
7.5.4
4.4.5
7.5.2
7.5.2
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                                                                                                                                                                                                                                                                                                                Sequence 4, Appli
Sequence 10, Appl
Sequence 1076, Ap
Sequence 4304, Ap
Sequence 2, Appli
Sequence 1981, Ap
Sequence 1981, Ap
Sequence 378, Appl
Sequence 378, Appl
Sequence 20, Appl
Sequence 20, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1670, Ap
Sequence 20241, A
Sequence 3471, Ap
Sequence 20536, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Appli
                                                                                            October 30, 2003, 00:01:13; Search time 310.043 Seconds (without alignments) 8070.528 Million cell updates/sec
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                                                                                                                                                        US-09-462-816-1
920
1 tgcaaacatgtccaaaaaca.....gtagttattaaaaaaaaa 920
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                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_MEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/USO8_WUB.Seq:*
16: /cgn2_6/ptodata/1/pubpna/USO8_WUB.Seq:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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10 US-09-844-645-4

12 US-09-824-645-4

12 US-09-878-574-4304

10 US-09-878-574-4304

11 US-10-311-455-1076

12 US-10-017-161-1981

12 US-10-017-161-1981

12 US-10-240-485-82

12 US-10-240-485-378

12 US-10-240-455-378

12 US-10-240-455-378

12 US-10-239-676-12

14 US-10-239-676-12

15 US-10-311-455-1670

9 US-09-864-761-3471

12 US-10-029-386-20536
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                   1811591 seqs, 1359896290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 4296, Ap Sequence 4109, Ap Sequence 1924, Ap Sequence 1924, Ap Sequence 1924, Ap Sequence 4312, Ap Sequence 675, App Sequence 678, App Sequence 2513, Ap Sequence 2013, Ap Sequence 1241, Ap Sequence 1783, Ap Sequence 1857, App Sequence 1857, App Sequence 1857, App Sequence 165, App Sequence 165, App Sequence 165, App Sequence 1793, Ap Sequence 1793, Ap Sequence 268, Appl Sequence 1123, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09847173
Publication No. US20020182228A1
GENERAL INFORMATION:
GENERAL THORMATION:
APPLICANT: Collins, Peter L.
TITLE OF INVENTION: PRODUCTION OF INFECTIOUS RESPIRATORY
SYNCYTIAL VIRUS FROM CLONED NUCLEOTIDE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
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SITAIR: CAR

COUNTRR READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/847,173
FILING DATE: 03-May-2001
CLASSIFICATION NUMBER: 08/720,132
PILING DATE: cluknown>
PRIOR APPLICATION NUMBER: 08/720,132
PILING DATE: cluknown>
MAMB: PROFENT INFORMATION:
NAMB: Parmele, Steven W.
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECAK: 415-576-0300
INFORMATION FOR EQUID NO: 1:
SECTIONE: CLUB NO: 1:
SECTIONE FOR EQUID NO: 1:
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CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
US-09-878-574-4296
US-09-884-761-19241
US-09-864-761-19241
US-09-864-761-19241
US-09-864-761-2513
US-09-864-761-2513
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US-09-878-574-4312
US-10-311-455-675
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                           301 AATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCACATACTAGCTTCAAC
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                                                                                                                                                                                         CACTCTCAATCATTATTATTCATATCATCGGGCTTATATAAAGTTAAAATCTGT
                                                                                                            Gaps
                                                                                 DB 10, Length 15223;
                                                                                                          ;
                                                                                                          Indels
                                                                                Score 853.4; DB 10;
Pred. No. 1.8e-210;
0; Mismatches 41;
  ;
TOPOLOGY: linear

MOLECULE TYPE: other

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-847-173-1
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STRANDEDNESS: single
                                                                                Query Match 92.8%;
Best Local Similarity 95.5%;
Matches 878; Conservative (
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69.3%; Score 637.4; DB 10; Length 696;
Best Local Similarity 96.1%; Pred. No. 3.7e-155;
Matches 664; Conservative 0; Mismatches 26; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                       APPLICANT: STILES, David E. McDaniel, Larry S. Curiel, David T. Curiel, David T. TITLE OF INVENTION: COMPOSITION AND METHODS FOR ADMINISTERING PNEUMOCCCCAL.
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2450
TELECOMMUNICATION INPORMATION:
TELESHONE: (212) 840-3333
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,645
FILING DATE: 27-Apr-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,505
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECILE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-844-645-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Frommer, William S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
Sequence 4, Application US/09844645
Patent No. US20020102242A1
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                    NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: U.S.A.
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: BOJ.1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
                                                                                                                                                                        191 ATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGC 250
                                                                                                                                                                                                                                                 251 CAGATCAAGAACACACAACATACCTCACTCAGGATCCTCAGCTTGGAATCAGCTT 309
                                                                                                                                                                                                                                                                                     310 CTCCAATCTGTCTGAAATTACATCACAAAC-CACCACATACTAGCTTCAACAACACCAG 368
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                                                                                                   Length 793;
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                                                                                               Query Match 9.3%; Score 85.8; DB 10; Length Best Local Similarity 48.4%; Pred. No. 4e-12; Matches 283; Conservative 0; Mismatches 300; Indels
; LOCATION: (1)..(793)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-C11
US-09-878-574-4304
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Publication No. US20030186277A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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; LOCATION: (379615)
US-10-312-841-2
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LENGTH: 3673778
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and other Molecules Associated with
TITLE OF INVENTION: Dants
FILE REFERENCE: 38-21(15401) B
CURRENT APPLICATION NUMBER: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR PILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 4304
LENGTH: 793
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                                                                           3;
                                     Length 7758;
                                   9.4%; Score 86.2; DB 12; Length 47.8%; Pred. No. 9.9e-12; ative 0; Mismatches 338; Indels
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                                                                         Matches 312; Conservative
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                                                       Similarity
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US-09-878-574-4304/c
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NAME/KEY: unsure
US-10-311-455-1076
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128 ATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATA 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     714 ATCAACAACAACAATAACAACAACAACAACCATAGCAACAATTACATCACCACAACA 773
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9.2%; Score 84.2; DB 12;
Best Local Similarity 45.4%; Pred. No. 1.6e-11;
Matches 350; Conservative 0; Mismatches 418;
                                                                                                                                                                                                                               g, unknown or other
                                                                                                                                                                                                                                                                                              LOCATION: (1319)..(1328)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                               ϋ
                                                                        FRATURE:
NAME/KEY: CDS
LOCATION: (201)..(1772)
FRATURE:
NAME/KEY: modified base
LOCATION: (975)..(994)
OTHER INFORMATION: a, t, c
                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: modified_base
                                                         (1)..(1972)
                                     source
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       FEATURE:
NAME/KEY:
LOCATION:
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                                                                                                                      2435804 CTCAACAAAACCTACAAAACACGAAAAAAAAAAAAACTCCACTAACCAATAAAAACACCACACCC 2435745
                                                                                                                                                                                                                   2435205 CCTCAACAAAACCTACAAAACACGCAAAAAAACTCCACTAACCAATAAAACACCACAT 2435146
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al Similarity 47.0%; Pred. No. 2.8e-10; 334; Conservative 0; Mismatches 372; Indels
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CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR PELING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
LENGTH: 1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1981, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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US-10-017-161-1981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 TITCACTICGAAGIGITIAACTITIGIACCCIGCAGCAIAIGCAGCAACAAICCAACTIC
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LOCATION: (4003, 5529, 5534, 5553, 5570, 5573, 5577..5578, 5592, 5732)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.8%; Score 81.4; DB 12; Length 16167;
46.6%; Pred. No. 2.5e-10;
tive 0; Mismatches 269; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) FEATURE:
                                                                                                 US-10-240-485-82/c

; Sequence 82, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: OLEK, Alexander
; APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: Metastasis
; FILE REPERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT PILING DATE: 2002-10-02
; PRIOR FILING DATE: 2001-04-06
; PRIOR PILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR PILING DATE: 2000-04-07
; PRIOR PILING DATE: 2000-06-07
; RRIOR PILING DATE: 2000-06-07
; RUMBER: OF SEQ ID NOS: 202
5386 AAAAAAAAAATAAAATCTCCTCC 5363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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                               Sequence 1056, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander

APPLICANT: PIEERNARCK, Christian
APPLICANT: PIEERNARCK, Christian
APPLICANT: BERLIN Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: 1014
TITLE OF INVENTION: 2010-10-16
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424
SEQUENCE OF SEQ ID NOS: 2424
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OTHER INFORMATION: n is a or g or c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
Local Similarity 46.6%; Pred. No. 2.5e-10;
Les 235; Conservative 0; Mismatches 269; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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) LCCATION: 5837..5838

CTHER INFORMATION: n is a or g or c or t

US-10-311-455-1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 16167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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APPLICANT: DIEK, AHEARANIAN:
APPLICANT: DIEK, AHEARANGET
APPLICANT: DIEK, AND
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Diagnosis of Diseases Associated
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: Dy Means of Assessing the Methylation Status of Genes Associat
TITLE OF INVENTION: With DNA TRANSCRIPTION
TITLE OF INVENTION: With DNA TRANSCRIPTION
TITLE OF INVENTION: WITH DNA TRANSCRIPTION
FILE REFERENCE: 5013.1009
CURRENT PRILING DATE: 2001-04-06
FRIOR APPLICATION NUMBER: DE 10019058.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR PILING DATE: 2000-04-06
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10032529.7
FRIOR PILING DATE: 2000-06-30
FRIOR PILING DATE: 2000-06-30
FRIOR FILING DATE: 2000-06-01
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llarity 45.1%; Pred. No. 2e-10;
Conservative 0; Mismatches 415; Indels
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; Sequence 20, Application US/10240453
; Publication No. US20030148326A1
; GENERAL INFORMATION:
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734 ATCACAACTACACTGCTCACCAACAACGCACAGGAAATCCAAAAGCTCACAAGTCAAATG 793
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Similarity 45.1%; Pred. No. 2e-10;
15; Conservative 0; Mismatch...
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As:
TITLE OF INVENTION: Cytosine methylation
FILE REPREBENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 378
                                                                                                                               794 GAAACCTTCCACTCAACCTCCTCC 817
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; Publication No. US20030143606A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-10-311-455-378/c
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Sequence 1670, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BEFEIN, Kurt
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT PRILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
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    Matches 345; Conservative
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US-10-311-455-1670/c
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Publication No. US20030082609A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: BIEPERBROCK, Christian
FILE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
DE 10019058.8
DE 10019058.8
DE 10019058.9
DE 1003252.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
2000-04-06
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2000-06-30
CTTAATCCCTAACCAAAAATATCCCCAACTACTAAATAACCAAAAATCGCCTTTCTCT 1577
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Pred. No.
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ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 228
SEQ ID NO 12
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Best Local Similarity
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US-10-239-676-12/c
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128 ATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATA 187
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OTHER INFORMATION: MAP TO ACO06547.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.6
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
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                                               PRIOR APPLICATION NUMBER: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1:1
PRIOR PILING DATE: 2001-01-29
NUMBER: DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-29
                                       WG DATE: 2000-09-27
ICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Matches
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica x.1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PLICATION NUMBER: US 60/180,312
PRIOR PLICATION NUMBER: US 60/207,456
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-06-36
PRIOR PRILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
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                                                                                                                                                                OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                 Length 6668;
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48.9%; Pred. No. 3.7e-10;
tive 0; Mismatches 225; Indels
                                                                                                                                                                                                                             NAME/KEY: unsure
CCATION: 1936
CTHER INFORMATION: n is a or g or c or
US-10-311-455-1670
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Patent No. US20020048763A1
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                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1670
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 48.99
Matches 215; Conservative
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8.5%; Score 78.2; DB 9; Length 1973;
Best Local Similarity 46.6%; Pred. No. 5.9e-10;
Matches 354; Conservative 0; Mismatches 398; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
PRATURE: NORMATION: MAP TO ACO06547.9
OTHER INFORMATION: EXPRESSED IN LUNG. SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.6
OTHER INFORMATION: EXPRESSED IN HEAA, SIGNAL = 9
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OTHER INFORMATION: EXPRESSED IN HEAA, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN FITAL LIVER, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN FITAL LIVER, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN MOUTH LIVER, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2000-09-21

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2001-01-29

PRIOR PILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

SEQ ID NO 3471

LENGTH: 1973
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US-09-864-761-3471
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APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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607
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELLOR INUMBER: US 60/180,312
PRIOR PELLOR ON NUMBER: US 60/180,312
PRIOR PELLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-09-37
PRIOR FILING DATE: 2000-10-04
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PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PPLICATION NUMBER: PCT/US01/00662
ILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
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Patent No. US20020048763A1
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Search completed: October 30, 2003, 03:23:48
Job time : 319.043 secs

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Sequence 3, A Sequence 3, A Sequence 14, Sequence 14,

Sequence Sequence Sequence

Sequence 1 Sequence 1 Sequence 1

US-08-836-504A-3 US-08-836-501-3 US-09-654-289-3 US-09-628-876-3 US-08-810-3 US-08-810-14 US-08-836-501-14 US-09-654-289-14 US-09-654-289-14 US-09-654-289-14 US-09-651-14 US-09-651-14 US-08-8177-12 US-08-836-501-23 US-08-654-289-23 US-09-654-289-23 US-09-654-289-23 US-09-654-28

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Sequence Sequence Sequence

ALIGNMENTS

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October 29, 2003, 21:37:29; Search time 71.4618 Seconds (without alignments) 5682.373 Million cell updates/sec
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/cgm2_6/ptodata/2/ina/5B_COMB.seq:*
/cgm2_6/ptodata/2/ina/6A_COMB.seq:*
/cgm2_6/ptodata/2/ina/6B_COMB.seq:*
/cgm2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgm2_6/ptodata/2/ina/PCTUS_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-467-964A-7

US-08-467-965A-7

US-08-467-965A-7

US-08-001-554A-7

US-08-001-554A-7

US-08-852-344D-28

US-08-852-344D-28

US-08-852-344D-28

US-08-852-344D-28

US-08-892-403A-1

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US-08-892-403A-1

US-08-836-501-1

US-09-626-830-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                        Sequence:
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GENERAL INPORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: KLEIN, Michel H
APPLICANT: DU, Run-Pan
APPLICANT: DU, Run-Pan
APPLICANT: DU, Run-Pan
APPLICANT: BKASYSHYN, MATY E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,189
FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR PEPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
ANDE: STEWART Michael IN RORMATION:
NAME: STEWART, Michael IN REPERENCE/DOCKET NUMBER: 1038-474 MIS:jb
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
Sequence 7, Application US/08467963C
Patent No. 5968776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID No. 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 920 base pairs
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STRANDEDNESS: single
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US-08-467-963C-7
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Appli Appli Appli Appli Appl

Sequence Sequence

15222 15222 15222 15222 15223 15223 1050 1050 303

853.4 8853.4 8853.4 8653.4 813

Sequence

Sequence Sequence

Sequence 28, Sequence 7, Sequence 7, Sequence 7, Sequence 7,

Sequence

Sequence

Sequence Sequence Sequence Sequence 1 Appl Appl Appl Appl Appl

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US-08-721-979A-3

Patent No. 5998169

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Length 920;
                    Indels
100.0%; Score 920; DB 2; I 100.0%; Pred. No. 8.8e-243;
                     0; Mismatches
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Query Match
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Matches 920; Conservative
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RESULT 2 US-08-838-189D-7 ; Sequence 7, Application US/08838189D

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GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: DV, Run-Pan
APPLICANT: BMASYSHYN, Mary E
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCACCATACTAGCTTCAAC
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                                                                                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 920; DB 2; I Best Local Similarity 100.0%; Pred. No. 8.8e-243; Matches 920; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION NUMBER: GB 9200117.1
PRIOR APPLICATION WUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 1038-687 MIS:jb
TELECHOMENICATION INFORMATION:
TELEFAX: (416) 595-1165
TELEFAX: (416) 595-1165
TELEFAX: (416) 595-1165
TELEFAX: (416) 595-1165
TELEFAX: (416) 295-1165
TELEGATH: 920 base pairs
TENGTH: 920 base pairs
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US-08-838-189D-7
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                        ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-688 MIC
TELECOMMUNICATION INFORMATION:
TELEPHORE: (416) 595-1155
TELERAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: MICHAEL 20 base pairs
                 GB 9200117.1
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 920; Conservative
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: KLEIN, Michel H
APPLICANT: EWASYSHYN, MAY E
TITLE OF INVENTION: CHIMBER PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Obtain

STATE: Obtain

COUNTRY: Canada

ZIP: MSG 1PF.
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

CORPATER: PER PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/852,344D

FILING DATE: 07-MAY-1997

CLASSIFICATION NUMBER: US/08/852,344D

FILING PAPLICATION NUMBER: US/08/852,344D

FILING DATE: 14-NOV-1994
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6th Floor, 330 University Avenue
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Patent No. 6017539
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STATE: Ontario
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100.0%; Pred. No. 8.8e-243;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        Sequence 7, Application US/08344639E

Batent No. 6033668

GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Klein, Machel H
APPLICANT: Bwasyshyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/344,639E
FILING DATE: 14-NOV-1994
CLASSIFICATION: A24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 424
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 66-JAN-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MACHARI I
REGISTRATION NUMBER: 1038-391 MIS
TELECOMMINICATION NUMBER: 1038-391 MIS
TELECOMMINICATION NUMBER: 1038-391 MIS
                                                                                                                                                                                                                                                                                                                                                                                                                                      330 University Avenue, 6th Floor
                                                                                                                                       GTAGTTATTAAAAAAAA 920
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TELEFAX: (416) 595-1163
TELER: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO. 7.
SEQUIENCE CHARACTERISTICS:
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Best Local Similarity 100.0
Matches 920; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Toronto
STATE: Ontario
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Patent No. 6168786
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Bwasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
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999 720 720 780 780 840

540 600 99

99

909

720

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661 AACCACTAAACCAAAGGAAGTACCCACCACCAAGCCCACAGAAGAGCCAACCATCAACAC 720
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                                                                                                                                                       601 CACCACCAAGCCTACAAAAAACCAACCTTCAAGACAACCAAAAAAGATCTCAAACCTCA
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Sequence 7, Application US/08467961A

Patent No. 6171781

APPLICANT: Klein, Michel H

APPLICANT: Nun-Pan

APPLICANT: Ewasyshyn, Mary E

TITLE OF INVENTION: Chimeric Immunogens

NUNBER OF SEQUENCES: 21

CORRESPONDENCES: 22

ADDRESSEE: Sim & MCBurney

STREET: 330 University Avenue, 6TH Floor

CITY: Toconco

STATE: Oncario

COUNTRY: Canada

ZIP: MGG 1R7

COMPUTER: EABDABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/467,961A

FILING DATE: 06-JUN-1995

CLASSIFICATION NUMBER: US 08/001,554

FILING DATE: 06-JAN-1993

CLASSIFICATION NUMBER: US 08/001,554

FILING DATE: 06-JAN-1993

PRIOR APPLICATION NUMBER: US 08/NO1,554
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILLING DATE: 06-JAN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart Michael
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                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,969A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR 
                             ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1038-475 MIS:bh
                                                                                                              STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGIESTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCE
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CATCATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGA 240
781 CACAAGTCAAATGGAAACCTTCCACTCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCA 840
                                                                                                                                                                                                                                                                                                                                                                    330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-286
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
TELERX. 065-24567 SIMBAS;
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
                                                                                             GTAGTTATTAAAAAAAA 920
                                                                                                                                                                                                     ; Sequence 7, Application US/08001554A; Patent No. 6225091
                                                                                                                          901 GTAGTTATTAAAAAAAAA 920
                                                                                                                                                                                                                                                     APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasysbyn, Mary E
TITLE OF INVENTION: Climeric In
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                        Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 920, Conservative
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                                                                                                                                                                                                                                                                                                                                                                  STREET: 330 Unive
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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US-08-001-554A-7
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                                                                                                                                                                                                                                          100.0%; Score 920; DB 3; Length 920; 100.0%; Pred. No. 8.8e-243; ive 0; Mismatches 0; Indels
           REFERENCE DOCKET NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
TELER: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: mucleic acid
STRANDENNES: single
 REGISTRATION NUMBER: 24,973
                                                                                                                                                      STRANDEDNESS: SINGLE TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                         Best Local Similarity 100. Matches 920; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
#PPLICATION NUMBER: US/08/001,554A
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
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Pred. No. 1.2e-235;
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                     97.2%; Scor.
100.0%; Pred. No. 1.
         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
FILING DATE:
                                                                                                                                                                                                                                                       LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 894; Conservative
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US-08-467-963C-28
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APPLICANT: KLEIN, Michel H
APPLICANT: EMASYSHYN, Mary E
APPLICANT: DU, Run-Pan
APPLICANT: DU, Run-Pan
APPLICANT: DO, Run-Pan
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMERIC PROTRIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
                                                                                                                                                CACAAGTCAAATGGAAACCTTCCACTCAACCTCCCAAAGGCAATCTAAGCCCTTCTCA
                                                                                                   AACACCAGGAGTCAAACCTGCAACCCACAACACTCAAGACTAAAAACACAACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/08467963C
Patent No. 5968776
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ADDRESSEE: Sim & MCB
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
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US-08-467-963C-28
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                                                                        1 ATGTCCAAAAACAAGGACCAACGCACGCTAAGACACTAGAAAAGACCTGGGGACACTCTC
                                                                                                                  68 AATCATTTATTATTCATCCAGGCTTATATAAGTTAAAATCTTAAAATCTGTAGCACAA
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61 AATCATTTATTATTCATATCATCGGGCTTATATAAAGTTAAATCTTAAATCTGTAGCACAA
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                          1 ATGTCCAAAAAACAAGGACCAACGCACCGCTAAGACACTAGAAAAAAGACCTGGGACACTCTC
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                                                                                                                                                128 ATCACATTATCCATTCTGGCAATGATAATCTCCAACTTCACTTATAATTACAGCCATCATA
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APPLICANT: DU, Run-Pan
APPLICANT: DV, Run-Pan
APPLICANT: DV, Run-Pan
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 37
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US-08-852-344D-28
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APPLICANT: KLEIN, Michel H
APPLICANT: EWASYSTRYN, Mary E
APPLICANT: BWASYSTRYN, MULTIMERIC HORDERS ENCODING A
TITLE OF INVENTION: CHIMBERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: CHIMBERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: TOTORIO
STRATE: Ontaxio
COUNTRY: Canada
                                                                                                                                                                                                                      781 CAAATGGAAACCTTCCACTCCACTCCCGAAGGCAATCTAAGCCCTTCTAAGTCTCCC
AAACCAAAGGAAGTACCCACCACCACCACAGAAGAGCCAACCATCAACACCACCAAA
                                                                           661 AAACCAAAGGAAGTACCCACCACCAAGCCCACAGAAGAAGCCAACCATCAACAACAAA
                                                                                                                                                    721 ACAAACATCACAACTACACTGCTCACCAACAACACCACGGAAATCCAAAAACTCACAAAGT
                                                                                                                                                                                                   CAAATGGAAACCTTCCACTCCACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCC
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:

NAME: STEWART, Michael I
REPRENEUCE/DOCKET NUMBER: 1038-687 MIS:jb
TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/08838189D Patent No. 5998169
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: MSG 1R7
COMPUTER READABLE FORM:
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US-08-838-189D-28
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607

667 99 727

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788 CAAATGGAAACCTTCCACTCAAACCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCC
          488 AATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCA
                                                                                                            668 AAACCAAAGGAAGTACCCACCACCAGCCCACAGAAGAGCCAAACCATCAACACCACCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                              728 ACAAACATCACAACTACACTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGT
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APPLICANT: Klein, Michel H
APPLICANT: Klein, Michel H
APPLICANT: BASSANA:
AND RESPIRATORY SYNCYTIAL VIRUS
ITILE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
ITILE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
ANDRESCE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BARDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BARDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BASABLE FORM:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: 1038-391 MIS
REFERENCE/DOCKET NUMBER: 1038-391 MIS
TELEFORME (416) 595-1155
TELEFORM: TELEFORM:
TELEFORM: (416) 595-1155
TELEFORM: TELEFORM
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Patent No. 6033668
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US-08-344-639E-28
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                                                                                                      STATE: Uncario
COMPUTRY: Canada
ZIP: M5G 1R7
COMPUTRY: READABLE FORM:
MEDIUM TYRE: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/M3-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,344D
FILING DATE: 07-MAY-1997
CLASSIFICATION ATA:
APPLICATION HOWER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION NUMBER: US 08/344,639
FILING DATE: 06-JMN-1992
ATORNEY/AGENT INFORMATION:
NAME: STEMARY, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-688 MIS:jb
TELECOMMUNICATION NUMBER: 1163
FILING CATAGENT INFORMATION:
TELECHONE: (416) 595-1163
INFORMATION FOR SEG ID NO: 28:
FILING SEQUENCE CHARRACTERISTICS:
TEMBERAX: (416) 595-1163
INFORMATION FOR SEG ID NO: 28:
FENCTH: R94 base pairs
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                 STATE: Ontario
                                        STREET: 6th r. CITY: Toronto
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,898A
FILING DATE: 18-FEB-1997
CLASSIPICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INPOSTATION:
NAME: Poissant, Brian M.
REGISTATION UNDRER: 28 465-
REFERENCE/DOCKET NUMBER: 8656-
TELECOMMUNICATION INFORMATION:
TELEFONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE GRARACTERISTICS:
LENGTH: 15222 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 95.5
Matches 878; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: RSV-A2
LOCATION: 1..15222
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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                                                                                                                                          Length 894;
                                                                                                                                          97.2%; Score 894; DB 3; Le
100.0%; Pred. No. 1.2e-235;
iive 0; Mismatches 0;
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                            Best Local Similarity 100.
Matches 894; Conservative
                                                                                          linear
                                                                                                         US-08-344-639E-28
                                                                                         TOPOLOGY:
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US-08-801-898A-23

Sequence 23, Application US/08801898A

Patent No. 598602

GENERAL INFORMATION:

APPLICANT: Torrence, Paul F.

APPLICANT: Silverman, Robert H.

APPLICANT: Cirino, Nick M.

APPLICANT: Li, Guiying

APPLICAN ö 120 240 61 CACTCTCAATCATTTATTCATATCATCGGGCTTATATAAGTTAAATCTTAAATCTGT 4681 TGCAAACATGTCCAAAAACAAGGACCAACGCACCGCTAAGGACATTAGAAAGGACCTGGGA 4741 CACTCTCAATCATTATTATTCATATCATGGCTTATATAAAGTTAAATCTTAAATCGG 121 AGCACAAATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTÄCAGC 4801 AGCACAAATCACTATTCTGGCAATGATAATCTCAACTTCACTTATAATTGCAGC 1 TGCAAACATGTCCAAAAACAAGGACCAACGCACCGCTAAGACACTAGAAAAGACCTGGGA 4861 CATCATATTCATAGCCTCGGCAAACCACAAAGTCACACCAACAACTGCAATCATACAAGA Gaps 92.8%; Score 853.4; DB 2; Length 15222; 95.5%; Pred. No. 5.4e-224; Live 0; Mismatches 41; Indels 0; ö

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RESULT 14
US-08-892-403A-1
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Sequence 12, Application US/08962690

GENERAL INFORMATION:
APPLICANT: TOTTENCH:
APPLICANT: Silverman, Robert H.
APPLICANT: Cirino, Nick M.
APPLICANT: Li, Guiying
APPLICANT: Li, Guiying
APPLICANT: Li, Guiying
APPLICANT: Li, Guiying
APPLICANT: Player, Mark R.
TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES
TITLE OF INVENTION: RPFECTIVE TO TREAT RSV INFECTIONS
FILE REFERENCE: 8656-019
CURRENT APPLICATION NUMBER: US/08/962,690
CURRENT FILING DATE: 1997-11-03
EARLIER APPLICATION NUMBER: 60/011,725
EARLIER APPLICATION NUMBER: 60/011,725
SARLIER PILING DATE: 1996-02-15
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 12
HAVELED IN O 12
                     ACCCAATAATGATTTTCACTTTGAAGTGTTCAACTTTGTACCCTGCAGCATATGCAGCAA
                                                                                                                      ACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTTGTACCCTGCAGCATATGCAGCAA
                                                                                                                                 CACCACCAAGCCTACAAAAAACCAACCTTCAAGACAACCAAAAAAGATCTCAAAACCTCA
                                                                                                                                                                  CACTACCAAGCCCACAAAAAACCAACCCTCAAGACAACCAAAAAAGATCCCAAAACCTCA
                                                                                                                                                                                                                      CACCAAAACAACATCACAACTACACTGCTCACCAACAACACCCACAGGAAATCCAAAACT
                                                      ; TYPE: DNA
; ORGANISM: respiratory syncytial virus
US-08-962-690-12
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US-08-962-690-12/c
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CACTCTCAATCATTTATTATTCATATCATCGTGCTTATATAAGTTAAATCTTAAATCTGT 10423
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                                       Gaps
   Length 15222;
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                                     Indels
                                     41;
 Score 853.4; DB 3;
Pred. No. 5.4e-224;
0; Mismatches 41;
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Query Match
Best Local Similarity 95.5%;
Matches 878; Conservative
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us-09-462-816-1.rni

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PATEUR NO. %2.04.95.7

SERBRAL INFORMATION:
APPLICANT: Collins, Peter L.
TITLE OF INVENTION: PRODUCTION PRESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS FROM CLONED NUCLEOTIDE SEQUENCES:
TITLE OF INVENTION: SYNCYTIAL VIRUS FROM CLONED NUCLEOTIDE SEQUENCES:
CREESPONDENCES.:
ADDRESSER: Townsend and Townsend and Crew LLP
STERET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
CUNTRY: US.A.
ZIP: 94111-3834
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/720,132
FILING DATE: Z7-SEP-1996
4922 TGCAACAAGCCAGATCAAGAACACACCCCAACATACCTCACCCAGAATCCTCAGCTTGG 4981
                                                                                                                                                                                                                                               5522 AGTCTCTACAACATCCGAGTACCCATCACAACCTTCATCTCCCACCAACACCACCCCAA
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                                           301 AATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCACCATACTAGCTTCAAC
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PRIOR APPLICATION DATA:
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US-08-720-132-1
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                                         APPLICANT: Murphy, Brian R.
APPLICANT: Multehead, Stephen S.
APPLICANT: Collins, Peter L.
APPLICANT: Miltehead, Stephen S.
APPLICANT: Unhasz, Katalin
TITLE OF INVENTION: PRODUCTION OF ATTENUATED RESPIRATORY
TITLE OF INVENTION: PRODUCTION OF ATTENUATED RESPIRATORY
CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1682 TGCAAACATGTCCAAAAACAAGGACCAACGCACCGCTAAGACATTAGAAAGGACCTGGGA 4741
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                                                                                                                                                                                                                                                                                                                                                  COMPIETE READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/892,403A

FILING DATE: 15-MUL-1997

CLASSIFICATION NUMBER: US 60/047,634

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/046,141

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/046,141

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/021,773

PRIOR DATE: 15-JUL-1996

ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 17634
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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  Patent No. 5993824
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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US 60/007,083

APPLICATION NUMBER:

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Search completed: October 30, 2003, 01:17:36 Job time : 74.4618 secs
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                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                    Score 853.4; DB 3;
Pred. No. 5.4e-224;
0; Mismatches 41;
FILING DATE: 27-58F-1995
ATTORNEY/AGENT INCORATION:
NAME: PARMELENCE STEWEN W.
REGISTRATION NUMBER: 31,990
REPREBUCE/DOCKET NUMBER: 15280-250-1
TELEPOMMUNICATION INFORMATION:
TELEPAN: 415-576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15223 base pairs
IENGTH: 15223 base pairs
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                    92.8%;
                                                                                                                                                                                                                                Query Match 92.8
Best Local Similarity 95.5
Matches 878; Conservative
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Respiratory syncyt Polymucleotide seq G protein gene fra Respiratory syncyt Respiratory syncyt Respiratory syncyt Human respiratory Syncyt Syncyt

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Sequence:

Searched:

Database

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PIV; RSV; multimeric; hybrid; pathogen; chimeric protein; vaccine;
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/label= Transmembrane anchor domain
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AAZ22911
AAZ22912
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AAX35270
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AAT31647
AAF84711
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(first entry)
feature
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13-JAN-1994
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HRSV glycoprotein
HSRV glycoprotein
                                                                            ; Search time 313.982 Seconds (without alignments) 7909.644 Million cell updates/sec
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1: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
5: /SIDSI/gcgdata/geneseqn-embl/NA1982.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
10: /SIDSI/gcgdata/geneseqn-embl/NA1980.DAT:*
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                                                                                                                                                                                                                                  5105512
          GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
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AAX08421
AAN10784
AAV18736
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AAT78440
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                 A novel multimeric hybrid gene is used as a vaccine. The gene consists of two gene sequences which are linked and encode antigenic regions, these two sequences being derived from two different pathogens (parainfluenza virus (PIV) and respiratory syncitial virus (RSV)). The gene sequences that are particularly used are those which encode PIV-3 F and HN proteins (AAQ45684) and RSV F and (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                               Indels
                                                                                    vaccines against multiple pathogenic infections e.g.
para-influenza virus and respiratory syncytial virus
                                                                                                                                                                                                                         Sequence 920 BP; 380 A; 290 C; 95 G; 155 T; 0 other;
                                                                           Multimeric hybrid genes and their chimeric proteins
                                                                                                                                                                                                                                           Score 920; DB 14;
Pred. No. 1.4e-211;
0; Mismatches 0;
                                                                                                                 Claim 11; Figure 7A-7D; 80pp; English.
                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 920; Conservative 0
         (CONN-) CONNAUGHT LAB LTD
                            Klein MH
                                              WPI; 1993-243222/30.
P-PSDB; AAR39286.
                           Ewasyshyn ME,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic composition for generating antibodies against respiratory syncytial virus - comprises non-replicating vector containing the protein g sequence, useful in protective vaccines and to raise antibodies for diagnosis
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 administered to a host organism. The composition is useful as a vacchine to immunise against RSV-associated disease, particularly resulting in a balanced Th1/Th2 immune response and for raising by usual immunisation and cell fusion methods.
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                                                                  100.0%; Score 920; DB 20; Length 920; 100.0%; Pred. No. 1.4e-211; ive 0; Mismatches 0; Indels 0.
                                                Sequence 920 BP; 380 A; 290 C; 95 G; 155 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccines for human respiratory virus - comprising proteins or fragment encoded by a DNA sequence coding for human respiratory syncytial virus proteins.
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                                                                                                                                                 Sequence encoding human respiratory syncytial virus (HRSV) A2
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Pred. No. 1.4e-196;
0; Mismatches 39;
                                                                                                                                                                                                             Human respiratory syncytial virus (HRSV)
                                                                                                                                                                                                                                   Location/Qualifiers
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Best Local Similarity 95.8%;
Matches 881; Conservative
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P-PSDB; AAP70845.
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05-APR-1991
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                                                                                                                              Production of human respiratory syncytial virus glyco-protein F or ( - by culturing eukaryotic host cells transfected with corresponding {\sf DNA}_{\sf N}
                                                                                                                                                                                           The present sequence was used in the development of a novel method for the production of human respiratory syncytial virus (HRSV) glycoprotein F (gpF) or glycoprotein G (gpG). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV gpF or gpG. The gp can be used to prepare vaccines against HRSV.
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                                                                                                                                                                                                                                                                                       935;
                                                                                                                                                                                                                                                                                   Score 857.6; DB 19; Length
Pred. No. 1.4e-196;
0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                Sequence 935 BP; 383 A; 293 C; 100 G; 159 T; 0 other;
                                                                                                                                                                         Example 1; Columns 27-28; 17pp; English
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           86US-0818740.
86WO-US02756.
92US-0897171.
97US-0854783.
                                                                                                                                                                                                                                                                                    Query Match 93.2%;
Best Local Similarity 95.8%;
Matches 881; Conservative
                                                             (PHAA ) PHARMACIA & UPJOHN
                                                                                 Wertz GW
                                                                                                   WPI; 1998-144802/13.
P-PSDB; AAW47605.
           14-JAN-1986;
23-DEC-1986;
11-JUN-1992;
12-MAY-1997;
                                                                                 Collins PL,
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                                          AATCAGTCCCTCTAATCCGTCTGAAATTACATCACAAAATCACCACCATACTTCAAC
                                                                      AACACCAGGAGTCAAGTCAAACCTGCAACCCACAACAGTCAAGACTAAAAACACAAAAAC
                                                                                                             ACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTTGTACCCTGCAGCATATGCAGCAA
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CACTCTCAATCATTAATTATTCATATCATGTGCTTATATAAAGTTAAATCTTAAATCTGT 128
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                                                The sequences of mRNA encoding HRSV structural proteins are given in AAQ29622-26. The proteins are F, G, 22K, 9.5K and major capsid protein N. The sequences and encoded proteins are useful for preparing vaccines against HRSV. The vaccines can be used to confer immunity against respiratory tract infections on human subjects. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                               Query Match 93.0%; Score 856; DB 13; Length 935; Best Local Similarity 95.7%; Pred. No. 3.4e-196; Matches 880; Conservative 0; Mismatches 40; Indels
                                                                                                                                                      Sequence 935 BP; 382 A; 294 C; 100 G; 159 T; 0 other;
                         Disclosure; Page 18; 21pp; English.
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                                                                                                                            CACCAAAACAAACATCATAACTACACTCACCTCCAACACACACAGGAAATCCAGAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K; major capsid protein; N; 8s.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory syncytial virus strain A2
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/label= G_protein
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88US-0218737
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(first entry)
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P-PSDB; AAR25302.
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13-JUL-1988;
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4801 AGCACAAAATCACATTCTCTGGCAATGATAATTCTCAACTTCAACTTTATAATTGCAGC
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                                                           AATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCACCATACTAGCTTCAAC
                                                                                                                                                                                                                 361 AACACCAGGAGTCAAGTCAAACCTGCAACACCACAACAGTCAAGACTAAAAACACAACAAC
                                                                                                                                                                                                                                                                                                5101 AACTCAAACACAAACCCAACGCAACACAAAACAAAGCCAAAAACAAACCAAGCAA
                                                                                                                                                                                                                                                                                                                                ACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTTGTACCCTGCAGCATATGCAGCAA
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                                                                                                 421 AACCCAAACACACCGAGCAAGCCCACTACAAAACAACGCCAAAACAACCACCAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSV; vaccine; gene therapy; upper respiratory tract disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human respiratory syncytial virus strain A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Respiratory syncytial virus anti-genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT63430 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AGCACAAATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGC 180
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGCAAACATGTCCAAAAAAAAGGACCAACGCACCGCTAAGACACTAGAAAAGACCTGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence was used in the preparation of a novel polynuclectide, comprising an antisense oligonuclectide, with a hydroxy group at one end, that is complementary to 15-20 bases of the anti-genomic RNA strand of a respiratory syncytial virus (RSV), a linker attached to the OH-end of the antisense oligonuclectide and an oligonuclectide activator of RNaseL attached to the linker. The polynuclectide can be used to treat RSV infections, which can also be treated by administration of the antisense oligonuclectide, so as to form a complex with activated RNase L in vivo. The polynuclectide can be transported across the cell membranes without carriers or permeability agents, and once introduced destroys antisense target RNA. It also inhibits RSV infection in vitro in a superior manner to the conventional drug, ribavirin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide containing sequence anti-sense to region of RSV -
connected via a linker to an activator of RNaseL, used to treat RSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.8%; Score 853.4; DB 18; Length 15222; 95.5%; Pred. No. 3.2e-195; Live 0; Mismatches 41; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15222 BP; 5923 A; 2706 C; 2356 G; 4237 T; 0 other;
                                                                                                                                                                                                                                                            respiratory syncytial virus; inhibition; strain A2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Torrence PF,
                                                                                                                                                                                                                                Human respiratory syncytial virus strain A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Pages 47-51; 89pp; English
                                                                  909 GTAGTTACTTAAAAAAAA 928
                                            901 GTAGTTATTAAAAAAAA 920
                                                                                                                                                                                                                                                                                                     Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cirino NM, Li G, Silverman RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                              (CLEV-) CLEVELAND CLINIC FOUND (USSH ) US NAT INST OF HEALTH.
                                                                                                                                             AAT78440 standard; DNA; 15222
                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0011725.
                                                                                                                                                                                                                                                                                                                                                                                         97WO-US02531
                                                                                                                                                                                                                                                          Antisense oligonucleotide;
RSV; treatment; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 95.5
Matches 878; Conservative
                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-1997;
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                                                                                                                                                                       AAT78440;
                                                                                                                  RESULT 6
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CACAAGTCAAATGGAAACCTTCCACTCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCA
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                                                                                                                                                                                                            CACCACCAAGCCTACAAAAAAACCAACCTTCAAGACAACCAAAAAAGATCTCAAAACCTCA
                                                                                                                                                                           CACCAAAACAAACATCACAACTACACTGCTCACCAACAACACCACAGGAAATCCAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - useful to protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            respiratory syncytial virus (RSV) D46. The genome is negative-sense; the complete nucleotide sequence of the wild-type B-1 virus has also been determined (see AAV17552). A novel infectious recombinant RSV comprises a RSV genome or antigenome, a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P), a large polymerase protein (L), and a RNA polymerase elongation factor, where the recombinant RSV has at least two attenuating mutations, one of the mutations specifying temperature-sensitive (ts) substitution at amino acid Phe521,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the 5'-3' positive sequence nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSV; attenuation; vaccine; pneumonia; bronchiolitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Attenuated respiratory syncytial virus vaccines individuals against RSV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 188-195; 238pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               syncytial virus antigenome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human respiratory syncytial virus D46.
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96US-0021773.
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Whitehead SS;
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09-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCCAATAATGATTTTCACTTTGAAGTGTTCAACTTTGTACCCTGCAGCATATGCAGCAA 5221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                      Infectious respiratory syncytial virus particles - useful for treatment of RSV or gene therapy of upper respiratory tract diseases
                                                                                                                                                                                                                                                                      A human respiratory syncytial virus (RSV) anti-genome sequence (AAT63430) is the 5' to 3' positive-sense sequence of RSV; the genomitself is negative-sense. It was synthesised in segments by RT-PCR using intracellular RSV mRNA or genomic rRNA isolated from purified viruses as template. Restriction site markers were intoduced by incorporating the changes into the primers used for RT-PCR. The recombinant sequence can be expressed with a nucleocapsid protein, a large polymerase protein and an an uncleocapsid phosphoprotein, a large polymerase protein and an RNA elongation factor to produce isolated infectious RSV particles useful for generating vaccines against RSV. Recombinant RSV genome or antigenome can also be used as a vector for gene therapy of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18; Length 15223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15223 BP; 5921 A; 2704 C; 2361 G; 4236 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.8%; Score 853.4; DB 18
95.5%; Pred. No. 3.2e-195;
cive 0; Mismatches 41;
                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                          Claim 46; Page 43-51; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .larity 95.5%;
Conservative
            96WO-US15524
                                              95US-0007083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           upper respiratory tract.
                                                                                                                                                     WPI; 1997-212893/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 878; Conser
           27-SEP-1996;
                                              27-SEP-1995;
                                                                                                                Colling PL:
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Gln831, Met1169 or Tyr1321 in the RSV polymerase gene or a ts nucleotide substitution in the gene-start sequence of gene M2.
Also claimed are: (1) an isolated infectious RSV particle which comprises a recombinant RSV (anti) genome, N. P. and L proteins, a RNA polymerase elongation factor, where the (anti) genome is modified: (1) to ablate or modulate expression of a SH, NS1. NS2 or G gene or a cis-acting regulatory sequence; and (11) by a termination codon introduced within a selected gene, or by a change in sequence, position or presence of a GS or GB transcription signal relative to the selected gene; (2) an expression vector; and (3) an RSV strain selected from cpts RSV 248 (ArCC WR 2450), cpts 248/955 (ArCC WR 2450), cpts 248/955 (ArCC WR 2451), cpts 8XV 530 (ArCC WR 2452), cpts 530/1009 (ArCC WR 2451) or Cpts 530/1009 (ArCC WR 2452), cpts RSV 530 (ArCC WR 2455), or cpts 530/1009 (ArCC WR 2451) or B-1 cp-23 (ArCC WR 2455), or cpts 530/1009 (ArCC WR 2451) or B-1 cp-23 (ArCC WR 2455), or cpts 530/1009 (ArCC WR 2451) or B-1 cp-23 (ArCC WR 2455), or cpts 530/1009 (ArCC WR 2451) or B-1 cp-23 (ArCC WR 2455), or cpts 530/1009 (ArCC WR 2451) or B-1 cp-23 (ArCC WR 2455), or cpts 530/1009 (ArCC WR 2452) or B-1 cp-23 (ArCC WR 2455), or cpts 530/1009 (ArCC WR 2452), or cpts 530/1009 (ArCC WR 2452) or B-1 cp-23 (ArCC WR 2455), or cpts 530/1009 (ArCC WR 2450), or cpts 530/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.8%; Score 853.4; DB 19; Length 15223; 95.5%; Pred. No. 3.2e-195; Live 0; Mismatches 41; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15223 BP; 5921 A; 2704 C; 2361 G; 4236 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.5
Matches 878; Conservative
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                                                                                841 AGTCTCCACAACATCCGAGCACCCATCACAACCCTCATCTCCACCCAACACACGCCA
                  5402 CACCAAAACAACATCATAACTACTACTCACCTCCAACACCCACAGGAAATCCAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= g
/note= "creates SphI site in F/M2 intergenic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Infectious chimeric respiratory syncytial virus (RSV) produced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= d
/note= "creates Ncol site in N gene nontranslated
                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "creates Ncol site in N gene nontranslated
                                                                                                                                                                                                                                                                                                                                                                            /note= "single C insertion to create Afill site
in the NS2-N intergenic region"
replace(1139,A)
                                                                                                                                                                                                                                                                      RSV; vaccine; attenuation; pneumonia; bronchiolitis; mutant; ss.
                                                                                                                                                                                                                                                   Respiratory syncytial virus D46 5'-3' positive sense sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site in G/F intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site in G/F
                                                                                                                                                                                                                                                                                         Chimeric - Human respiratory syncytial virus Chimeric - Bacteriophage T7.
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/note= "creates StuI
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replace (1140,G)
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replace (5612, A)
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1099
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                                                                                                                                                                                                                                                                                                               Synthetic.
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variation
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                                                                                                                      sequence of human respiratory syncytial virus (RSV); the genome itself is negative-sense. This antigenome CDNA, termed D46, was synthesized in segments by RT-PCR using synthetic oligonucleotides as primers and intracellular RSV mRNA or genome RNA isolated from purified virions as template. The antigenome includes a S'-terminal noriviral Gtriplet contributed by the T7 promoter, 4 sequence markers (see AAA88745-47) at positions 1099 (which adds 1 nucleotide to the length), 1139, 5611 and 7559, a ribozyme and tandem T7 terminators, and a single norviral 3'-phosphorylated residue contributed to the 3' end by ribozyme cleavage. The invention provides an isolated infectious chimeric RSV comprising a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P), a nucleocapsid phosphoprotein (P), and a partial or complete RSV genome or antigenome of one RSV strain or subgroup virus. The chimeric RSV is a chifferent RSV strain or subgroup virus combined with a heterologous gene of a chifferent RSV strain or subgroup virus. The chimeric RSV is a chifferent such as pneumonia and bronchiolitis in infantes. The mutations. It is useful as a vaccine against RSV, which causes diseases such as pneumonia and bronchiolitis in infantes. The almune system of an individual is stimulated to induce procection against natural RSV infection, preferably in a multivalent manner to achieve protection against multiple RSV strains and/or subgroups.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
cloned nucleotide sequences, useful as a vaccine against diseases caused by the virus, such as pneumonia and bronchiolitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 92.8%; Score 853.4; DB 21; Length 15223; Best Local Similarity 95.5%; Pred. No. 3.2e-195; Matches 878; Conservative 0; Mismatches 41; Indels 0; (
                                                                                                           present sequence is that of the 5' to 3' positive-sense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15223 BP; 5921 A; 2705 C; 2361 G; 4236 T; 0 other;
                                                                Example 7; Page 262-268; 280pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                             5342 AACCACTAAATCAAAGGAAGTACCCACCACCACCAAGCCACAGAAGAGCCAACCATCAACAC
                                                                                                                                             CACCAAAACAAACATCACAACTACACTGCTCACCAAAACAACACCACAGGAAATCCAAAACT
                                                                                                                                                                                                  CACAAGTCAAATGGAAACCTTCCACTCCTCCTCCGAAGGCAATCTAAGCCCTTCTCA
                                                                                                                                                                                                                                                           661 AACCACTAAACCAAAGGAAGTACCCACCACCAAGAGCCCACAGAGAGCCAACCATCAACAC
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                            601 CACCACCAAGCCTACAAAAAACCAACCTTCAAGACAACCAAAAAAAGATCTCAAACCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a chimeric nucleic acid construct comprising: a nucleotide sequence adapted for protein expression in plants; and a respiratory syncytial virus (RSV) coding sequence encoding an RSV protein or an antigenic protein or peptide of RSV. The construct can be used to immunize animals and humans against respiratory syncytial virus. The use of transgenic plants to generate the antigen allows the production of greater amounts of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric, respiratory syncytial virus; RSV; immunize; ds.
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                                                                                                 CACTCTCAATCATTATTATTCATATCGGGCTTATATAAGTTAAATCTTAAATCTGT
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                                                 TGCAAACATGTCCAAAAACAAGGACCAACGCACGGCTAAGACACTAGAAAAGACCTGGGA
                                                                       TGCAAACATGTCCAAAAACAAGGACCAACGCACCGCTAAGACATTAGAAAGGACCTGGGA
                         Gaps
                        o;
 Length 918;
92.2%; Score 848.2; DB 22; Length
95.8%; Pred. No. 2.6e-194;
ive 0; Mismatches 38; Indels
                         Matches 871; Conservative
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The invention relates to a recombinant Sendai virus comprising an exogenous nucleic acid encoding a paramyxovirus (PMV) protein or its antigenic fragment. The virus may be administered in combination with an antiviral chemotherapeutic compound. Two or more viruses expressing different PMV proteins nay be co-administered. Compositions comprising the virus are useful for eliciting a humoral and/or comprising the virus are useful for eliciting a humoral and/or purther a recombinant Sendai virus comprising an exogenous nucleic acid encoding a second PMV protein is also administered and priming and/or consting humoral or cellular immune response comprises administering one or more of a recombinant or isolated PMV protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendai viral one or more of a recombinant or isolated PMV protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendai viral effective vaccine against hprv or RSV (the major causes of paediatric respiratory disease) and also to express any gene of interest in target cells, providing a positive medical impact on impaired cells. Mild-type globin gene transfer (i.e. gene therapy) into stem cells effects a cure for sickle cell disease or betathate sendai virus replicates at level that is high enough to impair decidin immunity, but does not cause any harm to human recipient. The present sequence encodes a respiratory syncytial virus (RSV) G procein (sequence encodes a respiratory syncytial virus fRSV) G procein (sequence encodes a respiratory syncytial virus fRSV) G procein (sequence encodes a respiratory syncytial virus fRSV) G procein (sequence encombinant virus of the invention.
                                                                                                                      RSV, de; G protein; heavily glycosylated protein; antianaemic; antiviral; vaccine; gene therapy; paramyxovirus; sendai virus; PWV; antiviral chemotherapeutic compound; humoral response; cellular immune response; hPIV; paediatric respiratory disease; globin gene transfer; sickle cell disease; beta-thalassaemia; human immunodeficiency virus infection; HIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant Sendai virus useful in vaccines to protect infection paramyxoviruses, comprises exogenous nucleic acid encoding paramyxovirus protein or its antigenic fragment
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Pred. No. 8e-192;
0; Mismatches 37; Indels 0;
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                                                                                    syncytial virus G protein DNA.
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                                                                                                                                                                                                                                                                                                                                                                                      "G protein"
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                               Human respiratory syncytial virus
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Best Local Similarity 95.9
Matches 860; Conservative
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AAS20145 standard; DNA; 897 BP

RESULT 11 AAS20145 ID AAS2 XX us-09-462-816-1.rng

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                                                                      ATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATA 187
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                                                                                                         TTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACA
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                                                                                                      AGCACAAATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGC
                                                                                                                            10416 AGCACAAATCACATTATCCATTOTGGCAATGATAATCTCAACTTCACTTATAATTGCAGC
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                                                                                                                                                                                                                             ACAACATCCGGGGTACCCATCACCATCATCTCCACCCAACACACCACGCCGGTAG 897
                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide sequence of RSV strain A2,
                                                                                                                                                                                                                                                                                                                           DNA; 15210
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                                                                                                                                                                                                                                                                                                                        AAX59703 standard;
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26-JUL-1999

AAX59703;

RESULT

10471

Gaps

9

41; Indels

Length 15210;

DB 20;

90.3%; Score 830.4; DB 20, 94.6%; Pred. No. 1.1e-189;

3; Mismatches

Local Similarity 94.6

Query Match Best Local Si Matches 869;

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1 TGCAAACATGTCCAAAAACAAGGACCAACGCACCGCTAAGACACTAGAAAAGACCTGGGA

120

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The specification describes a composition comprising a polynucleotide consisting of an antisense oligonucleotide containing a hydroxy group, complementary to the genomic or antisenomic strand of a negative-strand RNA wirus, and an activator of RNSse L. The polynucleotide is used to inhibit, or treat, infection by negative-strand RNA viruses, specifically respiratory syncytial virus (RSV) but also (para)influenza, mumps, and rables. The polynucleotide can cross cell membranes without requiring carriers or permeabilizing agents, and can selectively cleave the RNA targeted by the oligonucleotide. The present sequence represents
                                                                                                                                                                                                                                                                                                          New composition useful for inhibiting or treating infections against negative-strand RNA virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15210 BP; 4232 A; 2351 C; 2700 G; 5919 T; 8 other;
                                                                                                                                                                                                                                  PF;
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                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 98pp; English.
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                                                                                                                                              97US-0962690.
                Respiratory syncytial virus.
                                                                                                                                                                            CLEV-) CLEVELAND CLINIC
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                                                                                                                                                                                                                           Cirino NM, Li
                                                                                                            02-NOV-1998;
                                                                                                                                              03-NOV-1997;
                                                #09922742-A1
                                                                              14-MAY-1999
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produced may also comprise the signal peptide of tissue plasminogen activator (LPA). The recombinant vector may also comprise the signal peptide of tissue plasminogen activator (LPA). The recombinant vector may also comprise sequences immunoprotective ability. The resulting immunogenic composition will agenerate antibodies directed against the RSV G protein when administered to a host organism. The composition is useful as a vaccine to immunise against RSV-associated disease, particularly by usual immunisation and cell fusion methods.
                                 The respiratory syncytial virus (RSV) G protein can be used in vaccines by inserting the G protein gene into a non-replicating vector. The G protein is placed under the control of alternative
         Claim 8; Figure 3; 67pp; English
                                                                                                                                                                                                                     77.78;
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Matches 715, Conservative
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            10056 ACCCAATAATGATTTTCACTTTGAAGTGTTCAACTTTGTACCCTGCAGCATATGCAGCAAA
                                                           661 AACCACTAAACCAAAGGAAGTACCCACCAAGCCCACAGAAGAGAGCAACCATCAACAC
                                                                                                                                                     CACAAGTCAAATGGAAACCTTCCACTCAACCTCCGAAGGCAATCTAAGCCCTTCTCA
                                                                                                                                                                                                                                                        9756 CACAAGTCAAATGGAAACCTTCCACTCCAACTTCCTCCGAAGGCAATCCAAGCCCTTCTCA
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                                                                                                                                                                                     CACCAAAACAAACATCACAACTACACTGCTCACCAACAACACACAGGAAATCCAAAACT
                                                                                         Immunogenic composition for generating antibodies against respiratory syncytial vitus - comprises non-replicating vector containing the protein G sequence, useful in protective vaccines and to raise antibodies for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G protein; respiratory syncytial virus; RSV; recombinant vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine, immune response; immunogenicity, tPA; antibody tissue plasminogen activator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein gene fragment of respiratory syncytial virus.
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1..702
/*tag= a
/product= "Secreted G protein"
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                                    77.7%; Score 715; DB 20; Length 715; 100.0%; Pred. No. 2.5e-162; Artive 0; Mismatches 0; Indel8
Sequence 715 BP; 305 A; 240 C; 70 G; 100 T; 0 other;
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247 240

360 426 486 480 546 540 909 600 999 99

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AGCCAGATCAAGAACACAACCCCAACATACCTCACTCAGGATCCTCAGGTTGGAATCAGC 307
                                                                                                                       TTCTCCAATCTGTCTGAAATTACATCACAACCACCACCATACTAGCTTCAACAACACCA 367
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                                                                                                                                                                                                              GGAGTCAAGTCAAACCTGCAACCCACAACAGTCAAGACTAAAAACACAACAAC.AACCCA
                                                                                                                                                                                                                                                                  TAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCC
                                                                                                                                                                                                                                                                                                                                                                            Attenuated respiratory syncytial virus vaccines - useful to protect individuals against RSV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumonia; bronchiolitis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Respiratory syncytial virus genome.
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96US-0021773.
97US-0046141.
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Whitehead SS;
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09-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Such that when an in-frame fusion is made, the resultant fusion protein may be transported to, and anchored in, a mammalian cell membrane where it can be exposed to the host immune system.

Insertion of pneumococcal surface protein A (PspA) coding sequence created plasmid pKSD2601. Intramuscular immunisation of BALB/c created plasmid pKSD2601 induced protection against an otherwise lethal challenge with a capsular type 3 pneumococcus. A claimed plasmid for expression of pneumococcal epitope DNA in eukaryotic cells includes a promoter for driving expression in a eukaryotic cell ceg. HVM-IR). DNA encoding a leader sequence (e.g. of RSVG) and DNA encoding a pneumonoccal epitope such as PspA. The invention also provides a vaccine comprising the plasmid and a suitable carrier or diluent, and optionally one or more cytokines or DNA encoding them, or a bacterial delivery system. The vaccine is used to elicit an immunological response in a host, including humans, susceptible to pneumococcal infection or sepsis. The plasmid can also be used to express a pneumococcal epitope of interest in vitro.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is a portion of the respiratory syncytial virus glycoprotein G (RSVG) gene. It has been inserted into plasmid pcDNA3 (see AAV38297) to create plasmid pcT4. This plasmid contains a human cytomegalovirus immediate early promoter and the RSVG gene portion
                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid containing pneumococcal epitope for expression in eukaryotic cells - useful for eliciting immunological response to pneumococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                        RSV; glycoprotein G; pneumococcal surface protein A; PspA;
infection; Streptococcus pneumoniae; sepsis; otitis media;
meningitis; bacteraemia; pneumonia; vaccine; genetic immunisation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Indels
                                                                                                Respiratory syncytial virus glycoprotein G gene portion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 696 BP; 284 A; 211 C; 78 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                            ĽS;
                                                                                                                                                                                                                                                                                                                                                            McDaniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 1C; 47pp; English.
                   ВР.
Query Match
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This is the complete nucleotide sequence of the wild-type B-1 respiratory syncytial virus (RSV). The genome is negative-sense the 5'-3' positive-sense sequence of D46 is provided in AAV17553.

A novel infectious recombinant RSV comprises a RSV genome or antigenome, a major nucleocappia (N) protein, a nucleocapsid phosphoprotein (P), a large polymerase protein (L), and a RNA polymerase elongation factor, where the recombinant RSV has at polymerase elongation factor, where the recombinant RSV has at camperature-sensitive (ts) substitution at amino acid Phe521, a last temperature-sensitive (ts) substitution at amino acid Phe521, and class two attenuating mutations, one of the mutations specifying a temperature-sensitive (ts) substitution at amino acid Phe521, and claimed are: (1) an isolated infectious RSV particle which comprises a recombinant RSV (anti)genome, N, P, and I proteins, a RNA polymerase elongation factor, where the (anti)genome is modified: (1) to ablate or modulate expression of a SH, NSI, NS2 or G gene or a cis-acting regulatory sequence, or by a change in sequence, introduced within a selected gene, or by a change in sequence, the selected gene; (2) an expression vector; and (3) an RSV strain selected gene; (2) an expression vector; and (3) an RSV strain selected gene; (2) an expression vector; and (3) an RSV strain selected gene; (2) an expression vector; and (3) an RSV strain selected gene; (2) an expression vector; and (3) an RSV strain selected from cpte RSV 248 (ATCC WR 2453), cpts RSV 530 (ATCC WR 2452), cpts 530/1009 (ATCC WR 2451) or cpts 530/1030 (ATCC WR 2452), cpts 530/1009 (ATCC WR 2451) or cpts 530/1030 (ATCC WR 2452), cpts 530/1009 (ATCC WR 2453), cpts RSV 540 and RSV particles are used in a vaccine or communiant RSV and RSV particles are used in a vaccine protection and against MSV the expenses on vector of inforce protection or simulate the immune system of an individual to induce procedure. Sequence 15225 BP; 5904 A; 2710 C; 2399 G; 4212 T; 0 other; protection against RSV. The expression vector of (2) the production of infectious attenuated RSV particles. Example 4; Page 195-202; 238pp; English.

Ä 3; Gaps Query Match
48.0%; Score 441.4; DB 19; Length 15225;
Best Local Similarity 68.1%; Pred. No. 3.8e-96;
Matches 629; Conservative 0; Mismatches 291; Indels 3; C

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Perfect score:
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RESULT 1 A16257 LOCUS DEPINITION ACCESSION VERSION KEYNORDS SOURCE ORGANISM TEPERENCE AUTHORS TITLE JOURNAL		A16257 Synthetic J A16257.1 (Y A16257.1 (Synthetic of the synthetic of	r) r) r) at m (5-	NSV G gene 51:640933 Construct Sonstruct Requences. I to 920) AMUNOGENS	920 bp (seq ID No: 7) 7 22-JUL-1993;	DNA linear PAT 03-OCT-1994

CAAACATCACAACTACACTGCTCACCAACAACACCACAGGAAATCC CAAACATCACAACTACACTCACCAACAACACCACAGGAAATCC AAATGGAAACTTCCACTCAACCTCCTCGGAGGCAATCTAAGCCC CAACATCGGAAACCTTCCACTCTCTCCGAAGGCAATCTAAGCCC CAACATCGGAAACTTCCACTCAACCTCTCTCCGAAGGCAATCTAAGCCC CAACATCCGAGCACCCATCAACCTCTCTCCCACCCACAACCAAC	LUCUUS A16258 MIG2SA ACCESSION A16258 ACCESSION ACCESSION A16258 ACCESSION ACC	ich il Similari 920; Cons 920; Cons 1 TGCAAAC 1 TGCAAAC 61 CACTCTC 61 CACTCTC 60 CACTCTC 60 CACTCTC 60 AGCACAA 600 AGCACACA 600 AGCACAA 600 AGCACACAA 600 AGCACAA	0y 181 CATCATATTCATAGCCTCGGCAAACCACAAAGTCACAACTGCAATCATACAAGA 240 bb 740 CATCATATTCATAGCCTCGGCAAACCACAACACACACTAACAACTGCAATCATACAAGA 681 cy 241 TGCAACAAGCCAGATCAACACACCACACACACTCAACATCACATCATACATGG bb 680 TGCAACAAGCCAGATCAACACACACACACACACACACACA
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09 181 CATCATATTCATAGCCTCGGCAAACCACAAGTCACCTAACAACTGCAATCATACAAGA 240 181 CATCATATTCATAGCCTCGGCAAACCACAACAACAACAACAACAACAACAACAACAA		541 CAATCCAACCTGCTGGGCTATCTGCAAAGAATACCAAACAAA	DD 661 AACCACTAAACCAAAGGAAGTACCCACCCAGCAGAGGCCACAGAAGCCATCAACAC 720	RESULT 4 AR092530 LOCUS AR092530 SEFINITION Sequence 7 from patent US 5998169. ACCESSION AR092530. VERSION AR092530.1 GI:10019284 KEYWORDS SOUNCE UNKNOWN. ORGANISM UNKNOWN.	d)
Db S00 AACCCAAACACCAGCAAGCCCACTACAAAACAACGCCAAAACAAAC	320 CACCACCAAGCCTACAAAAAACCAACCTTCAAGACCAAAAAAAA	Db 140 Chchadrdchalccrrccharctrccharctrccharctrccharctrandccrrccrc Cy 841 AGTCTCCACAACATCCGACCCCATCCACCTCCTCCCACCAATCTAAGCCCTTCTCA Cy 801 GTACTACTAAAAAAAA 920 Cy 901 GTACTATTAAAAAAAAA 1 Db 20 GTAGTTATTAAAAAAAA 1	RESULT 3 AR080406 AR080406 AR080406 AR080406 BEFINITION Sequence 7 from patent US 5968776. ACCESSION AR080406 ACCESSION AR080406 ACCESSION AR080406	rce NT Match ocal S s 920	CTGGGA ATCTGT ATCTGT ATCTGT IACAGC

LOCUS AR122885 920 bp DNA linear PAT 16-MAY-2001	Ouery Match Best Local Similarity 100.0%; Pred. No. 3e-192; Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 1 TGCAAACATGTCCAAAACAAGGACCAACGGCTAAGACACAGAAAAAAAA	61 CACTCTCAATCATTATTATTACTCATCACGGGCTTATATAAGTTAAATCTTAAATCTGT 61 CACTCTCAATCATTATTATTCATCACGGGCTTATATAAGTTAAATCTTAAATCTGT 121 AGCACAAATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAAATTCTGGC	181 CAICATATICATAGE CICGOCARACCA CARACTICATAGE 240 181 CAICATATATACATACATAGE 240 181 CAICATATATACATACACACATACATACATAGE 240 181 CAICATATATACATACACAACACACACACACACACACACA	OY 301 AATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCCATACTAGCTTCAAC 360 301 AATCAGCTTCTCCCAATCTGTCTGAAATTACATCACAACCACCATACTAGCTTCAAC 360 OY 361 AACACCAGGAGTCAAACCTGCAAACCACAAACAACTAAAAAAACAACAACAACAACAACA	OY 421 AACCCAAACCACAAGCCCACTACAAAACAAACGCCAAAACAAAC	481 ACCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCAAGCA	OY 601 CACCACCAAGACTACAAAAAAACCAACCTTCAAGACAACCAAAAAAGATCTCAAAACCTC 660	Oy 661 AACCACTAAACCAAAGGAAGTACCCACCACCACACACACA	Oy 721 CACCAAACAACACACACACACGCCCCCCACACACACACA
Query Match 100.0%; Score 920; DB 6; Length 920; Best Local Similarity 100.0%; Pred. No. 3e-192; Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 TGCAAACATGTCCAAAACAAGACCAACGACCACGACACATAGAAAACTTGGGA 60 Db 1 TGCAAACATGTCCAAAAAAAAAAAAAAAAAAAAAAAAAA	Oy 181 CATCATATTCATAGCTCGGCAAACCACAAAGTCACACAACTGCAATCATACAAGA 240	301 AATCAGGAGTCCAATCTGTCTGAAATTACATCACACACAC	OY 11 ANCOCAARCAA 480 OY 421 AACCCAARCAACCAGCAACCACTACAAACAACCACAAAACAAA	OY 541 CAATCCAACCTGCTGGGTATCTGCAAAAGAATACCAAAAAAACCAGGAAAGAAA	Oy 661 AACCACTAAACCAAAGGAAGTACCCACCAACCAAGAAGAGCCAACCATCAACAC 720 Db	721 CACCAAACATCACAACTACACTGCTCACCAACAACACACAC	OY 841 AGTCTCCACAACATCCGAGCACCCATCACACCCTCATCTCCACCAACAACAACAACAA 900	Oy 901 GTAGTTATTAAAAAAAA 920 	RESULT 5 AR122885

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QY 541 CAATCCAACCTGCTGGGCTATCTGCAAAAGAATACCAAAAAAAA	CACCADACCADACATCACCACCACACACACACCACAGGAAATCCADAACT CACCADAACAAACATCACCACCACACACACCACAGGAAATCCADAACT CACCADAACAAACATCACTGCTCACCAACACACCACAGGAAATCCADAACT CACAAACTCAAATGGAAACTTACACTCACTCACCCAAGGCAATCTAAGCCCTTCTCA CACAAGTCAAATGGAAACCTTCCACTCACTCCCCAAGGCAATCTAAGCCCTTCTCA AGTCTCCACAACTCGAACCTTCCACTCAACCTCTCCCAAGGCAATCTAAGCCCTTCTCA AGTCTCCCACAACATCGAAGCACCCATCAACCTCTCACCCCACCAACACACCCCAACACCCCAACACCCCAACAC	RESULT 7 AR148357 LOCUS DEFINITION Sequence 7 from patent US 6225091, VERSION AR148357 VERSION AR148357.1 GI:15112447	Unknown. Unknown. Unclassif 1 (bases Klein, M.H Multimeri Protectio	SE COUNT 380 a 290 c 95 g 155 t IGIN Query Match Best Local Similarity 100.0%; Score 920; DB 6; Length 920; Best Local Similarity 100.0%; Pred. No. 3e-192; Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 1 TGCAAACATGTCCAAAACAAGGACCAACGGCTAAGACACAAAAAAAA	OY 61 CACTCTCAATCATTATTCATATCAGGGCCTCTAAGACACTGGAAAGCTGGGG 60 QY 61 CACTCTCAATCATTTATTCATATCAGGCTTATATAAAGTTAAATCTTAAATCTT 120 CACTCTCAATCATTTATTCATATCAGGCGCTTATATAAATCTTAAATCTTAAATCTTT 120 CACTCTCAATCATTATTCATACTCGGCAATGATAATCTCACTTATAATACTGG 180 DD 121 AGCACAAATCACATTATCCATTCTGGCAATGATAATCTCACTTATAATTACAGC 180 DD 121 AGCACAAATCACATTATCCATTCTGGCAATGATAATCTCACTTATAATTACAGC 180 CACTCTCAAATCATACCATTATCCATTCTGGCAATGATAATCTCACTTATAATTACAGC 180 DD 121 AGCACAAATCATTCATAGCCTCGGCAAAGCCAACCTAACAATCATAAATACAGG 240 DD 181 CATCATATTCATAGCCTCGGCAAACCACAACTAACAACACAACAACAAAGA 240 QY 241 TGCAACAAGCCAGAACCACAACCCCAACATCCTCAGGATCCTCAGGATCATGGG 300
Qy 781 CACAAGTCAAATGGAAACCTTCCACTCACCTCCTCCGAAGGCAATCTAAGCCCTTCTCA 840 Db 781 CACAAGTCAAATGGAAACCTTCCACTCCACTCCTCCGAAGGCAATCTAAGCCCTTCTCA 840 Qy 841 AGTCTCCACACAACATCCGAGCACCACCACCACCAACACAACACAACACAACACAACA	RESULT 6 AR123540 LOCAGO AR123540 DEFINITION Sequence 7 from patent US 6171783. ACCESSION AR123540 VERSION AR123540.1 GI:14108901 KEYWORDS SOURCE Unknown. ORGANISM Unknown. ORGANISM Unknown. TITLE Infection detection method using chimeric protein FEATURES LOCAGO AR123540 B20 DNA 11783-2001 FEATURES LOCAGO BAT 16-MAY-2001 AUTHORS LOCAGO BAT 16-MAY-2001 AUTHORS LOCAGO BAT 16-MAY-2001 AUTHORS LOCAGO BAT 16-MAY-2001 AUTHORS LOCAGO BAT 16-MAY-2001	<pre>source 1920 BASE COUNT 380 a 290 c 95 g 155 t ORIGIN Ouery Match Best Local Similarity 100.0%; Fred. No. 3e-192; Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	1 TGCAAACATGTCCAAAACAAGGACCACGCTAAGACACTGGAAAAGACTGGGA 60	QY 181 CATCATATTCATAGCCTCGGCAAACCACAAGTCACTAACAACTGCAATCATACAAGA 240 Db 181 CATCATATTCATAGCCTCGGCAAACCACAAGTCACTAACAACTGCAATCATACAAGA 240 Cy 241 TGCAACAAGCCAGATCAACACCCCAACATCCTCACTCACT	301 AATCAGCTTCTCCAATCTGTCTGCAACTCCAAACCACCACCATACTTCAAC 361 AACACCAGGAGTCAAGTCTGCAACTCGCAACCACCACCATACTAGATCAAC 361 AACACCAGGAGTCAAGTCAAACTGCAACCCACACACACAACAAC 421 AACACCAAACACAACCTGCAACCTGCAACAACAACAACAACAACAACAACAACAACAACAACAA

CC Nucleic acid vaccines encoding G protein of respiratory CC syncytial virus FH Key Location/Qualifiers FEATURES Location/Qualifiers 1920 1920 According G protein of respiratory CC (7)(901).	ncytiai t	y Match Local Simila hes 920; Co	TGCARACATGTCCAAAAACAAGGCCAAGGCACGCTAAGACACTAGAAAAGACCTGGGA 60 		121 AGCACAAATCACTTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTATCAGC 121 AGCACAAATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACCTTATAATTACAGC 121 ACCACAAAATCACATTATCTTCTGCCAATGATAATCACTTCAATTAATT	181 CATCATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAGA 181 CATCATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGA 181 CATCATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATAACAAGA	241 IGCARCAGGCAGATCAGGACCCCCAACATCACTCACCTCAGGATCCTCAGCTTGG	ON 301 AATCAGCTTCTCCAATCTGTGTGAATTCACACCACCAACCA	361 PACACCAGGGGTCAAACCTGCAACCGCAACGAAGACTAAAAACACAACAACAACAACAACAACAACAACAACAA	Qy 421 AACCCAAACACCAGCCAAGCCCACTACAAAACAAACAAAC	
	Oy 361 AACACCAGGAGTCAAACCTGCAACCAACAGTCAAGACTAAAAACACAAAAC 420	421 AACCCAAACACCAGCAAGCCCACTACAAAAGAAGGCGAAAACAAAC	481 ACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGGATATGCAGGAA 481 ACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCTGCAGGATATGCAGGAA	Qy 541 CAATCCAACCTGCTGGGTATCTGCAAAAGAATACCAAACAAA	OY 601 CACCACCAAGCCTACAAAAACCAACCTTCAAGACAACCAAAAAGATCTCAAACCTCA 660	QY 661 AACCACTAAACCAAAGGAAGTACCACCACCAACCACAGAAGACCAACCA	Qy 721 CACCAAAACAAACATCACTGCTCACCAACAACACCACAGGAAATCCAAAACT 780	OY 781 CACAAGTCAAATGGAAACCTTCCACTCAACCTCCTGAAGGCAATCTAAGCCCTTCTGA 840 Db 781 CACAAGTCAAATGGAAACCTTCCACTCAACCTCCGAAGGCAATCTAAGCCCTTCTGA 840	841 AGTCTCCACAACATCCGACCA 	OY 901 GTAGITATTAAAAAAAA 920 Db 901 GTAGITATTAAAAAAAA 920	BD081933 BD081933 BD081933 BD081933 BD081933 BD081933 BD081933 BD081933 ACCESSION Virus. ACCESSION BD081933.1 GI:22627543 BD081933.1 GI:22627543 BD081933.1 GI:22627543 BD081933.1 GI:22627543 BD081933.1 GI:22627543 BD081933.1 GI:2262741. BD081933.1 GI:22627543 BD081933.1 GI:226274. BD081933 BD0819333 BD08193333 BD08193

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309 AATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCATACTAGCTTCAAC 368	361 AACACCAGGAGTCAAGTCAAACCTGCAACCCACAACAGTCAAAAAACACAACAAC 420 	421 AACCCAAACACAACCAAGCAAGCCACTACAAAACAACGCCAAAAACAACACCACAAAAAAAA	489 ACCCATATTTCACTTCGAGGTTTTGTTTGTACCTGCAGCAGGGA 548 541 CAATCCACCTGCAGGTTTTCACAAAAAAAACAAAAAAAAA	601 CACCACCAAGCCTACAAAAACCAACCTTCAAGACCAACCA	661 AACCACTAAACCAAAGGAAGTACCACCACCACACACACAGAAGAGCCAACCATCAACCA 720	721 CACCAAAACATCACAACTACACTGCTCACAACAACAACAAGGAATCGAAAACT 780 	781 CACAAGTCAAATCGAAACCTTCCACTCAACCTCCGAAGGCAATCTAAGCCCTTCTCA 840	841 AGTCTCCACAACATCCGAGCACCCATCACAACCCTCATCTCCACCCAACACACAC	901 GTAGTTATTAAAAA 915 		ON Human respiratory syncytial virus (MON-7-91) subgroup A, glycoprotein. N Z33429 Z33429-1 GI:485888	KAYWOUNG G Gene; glycoprotein. SOURCE Human respiratory syncytial virus ORGANISM Human respiratory syncytial virus Viruses; sernA negative-strand viruses; Mononegavirales;	REFERENCE 1 (bases 1 to 912) AUTHORS Garcia,O., Martin,M., Dopazo,J., Arbiza,J., Fabrasile,S., Russi,J., Hortal,M., Perez-Brena,P., Martinez,I., Garcia-Barreno,B. and	Meleko, J.A. Evolutionary pattern of huma A): cocirculating lineages a changes in the G glycoprotei	94335057 94335057 8057427 2 (bases 1	ANIDAKS DEPAZO.T. TITLE Direct Submission JOURNAL Submitted (10-MAY-1994) Dopazo J., Centro Nacional de Biotecnologia - CSIC, Bioinformatica, Universidad Autonoma, Cantoblanco, Madrid, FRATURES Location/Qualifiers
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Db 841 AGTCTCCACAACATCCGAGCACCCATCACAACCCTCATCTCCACCAACAACAACAACGCCA 900	Cy 901 GTAGTTATTAAAAAAAAA 920 Db 901 GTAGTTATTAAAAAAAA 920	RESULT 9 HRSRNAG LOCUS HRSRNAG 923 bp mRNA linear VRL 24-JUN-1992 BEFINITION Human respiratory syncytial (RS) virus mRNA for G protein.	VERSION A17085.1 GI:60306 KEYWORDS G protein. SOURCE Human respiratory syncytial virus ORGANISM Human respiratory syncytial virus Viruses; ssRNA negative-strand viruses; Mononegavirales;	P	AL NE	ø	11250"	/product="G" protein" /protein id="CAA34937.1" /db_xref="G1:60307" /db_xref="SPTPRMR1.0199"	/trānslation="MSKNKOORTAKTLEKTWDTLAYLLFISSGLYKLNIKSIAQITLS ILAMIISTSLIITAIIFISSANHKVTLTTAIIQDATSQIKNTTPTYLGOPQLGISFS NLSSITTILASTTPGYKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPN NDFHPEVFNFVPCSICSNNPTCWAICKTIPRKTTTTTQTQPSKPTTKKPLFRQ THYKDPSVPROPPDPRIPETAINTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ANATASEHENDESETINITALINITALIAN TONEN AND SANDAY SQUATESEHENDESETINITALIAN TONEN AND SANDAY SANDA	Query Match Best Local Similarity 99.1%; Score 911.8; DB 14; Length 923; Best Local Similarity 99.8%; Pred. No. 1.9e-190; Matches 913; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Oy 1 TGCAAACATGTCCAAAAAGACCAAGGACGACGCTAAGAACACTAGAAAAGACTGGGA 60	Oy 61 CACTCTCAATCATTATTCATATCATCGGGCTTATATAAGTTAAATCTTAAATCGT 120	Oy 121 AGCACAAATCACATTATCCATTCTGGCAATGATAACTTCAACTTCACTTATAATACAGC 180	Oy 181 CATCATATTCATAGCCTCGGCAAACCACACACTCACACTAACAACTGCAATCATGAGA 240	OY 241 TGCAACAAGCCAGATCAAGAACCCCAACATACCTCACTCA

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NDFHFEVFRVPCSICSNNPTCWAICKRIPHKKAFTKKFTKKCHKROHKRO
TTKPKEVPTTKPTERFTINTTKTNIITTLINNTTGNPKLTSQMETFHSTSSEGNLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSHGLYG 917 bp ss-RNA linear VRL 03-AUG-19:
Human respiratory syncytial virus (subgroup A) attachment protein
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                                                     CACCAAAACAAACATCACAACTACACTGCTCACCAACAACAACCAAGGAAATCCAAAAACT
                                                                                                                                                                                                                       CACAAGTCAAATGGAAACCTTCCACTCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCA
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                       AACCACTAAACCAAAGGAAGTACCCACCACCAAGCCCACAGAAGAGCCAACCATCAACAC
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Onbnson, P.R., Spriggs, M.K., Olmsted, R.A. and Collins, P.L.
The G glycoprotein of human respiratory syncytial viruses
subgroups A and B: extensive sequence divergence between
antigenically related proteins
Proc. Natl. Acad. Sci. U.S.A. 84 (16), 5625-5629 (1987)
87289657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   attachment glycoprotein; surface glycoprotein.
Human respiratory syncytial virus
Human respiratory syncytial virus
Yiruses; ssRMA negative-etrand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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/note="attachement glycoprotein
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               /organism="Human respiratory syncytial virus"
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/isolate="MON 7 91 (Montevideo/Uruguay, 1991)"
/db_xref="taxon:11250"
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RESULT 12
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SOURCE
ORGANISM

Unknown.

REFERENCE AUTHORS TITLE

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68 AATCATTTATTCATATCATCATCGGGCTTATATAAGTTAAATCTTAAATCTGTAGCACAA
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100.0%; Pred. No. 1.6e-186;
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Patent: US 5968776-A 28 19-OCT-1999;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 894)
Klein,M.H., Du,R.-P. and Ewasyshyn,M.E.
Multimeric hybrid gene encoding a chimeric protein which confers
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661 AAACCAAAGGAAGTACCCACCACCACAGAAGAGCCAACCATCAACCACCACAA 720 728 ACAAACATCACAACTACACTGCTCACCAACAACACCAAGGAATCCAAAACTCACACAAGT 787 721 ACAAACATCACAACTACACTGCTCACCAACAACACACAGGAATCCAAAACTCAACATCACAACTTACAACATCAACATCAACATCAACATCAACATCAACATCAACATCAACATCAACATCCAACACTCCAACATCCAAGGCAATCTAAGCCCTTCTCAAGTCTCC 847 788 CAAATGGAAACCTTCCACTCCACCTCCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCC 847 781 CAAATGGAAACCTTCCACTCCACCTCCCGAAGGCAATCTAAGCCCTTCTCCAAGTCTCC 840 848 ACAACATCCGAGACCCCATCACACCTCTCCACCCAACACACAC	RSHICE 8510 bp ss-RNA linear VRL 29-NOV-2000 Human respiratory syncytial virus nonstructural protein (1C), nonstructural protein (1B), major nucleocapsid (N), phosphoprotein (P), protein (M), 1A (1A), G (G), protein (F) and envelope-associated protein (2X, gene, complete cds. MI1485 K01459 K02719 K03348 K03349 MI1217 MI1244 MI1487 MI1505			6310521 2 (bases 3211 to 4157) 2stake,M. and Venkatesan,S. Nucleotide sequence of the gene encoding respiratory syncytial virus matrix protein. 94138336 669948	3 (bases 2288 to 3191) Satake,M., Elango,N. and Venkatesan,S. Sequence analysis of the respiratory syncytial virus phosphoprotein General Section (1984) B5033973 A hasse for to 7500	Collins, P.L., Huang, Y.T. and Wertz, G.W. Nucleotide sequence of the gene encoding the fusion (F) Glycoprotein of human respiratory syncytial virus Proc. Natl. Acad. Sci. U.S.A. 81 (24), 7683-7687 (1984) 85088471 6096849 5. (bases 7551 to 8510)	Colling Fig. and Wertz, 1.5 The envelope-associated 22K protein of human respiratory syncytial virus: nucleotide sequence of the mRNA and a related polytranscript J. Virol. 54 (1), 65-71 (1985) S135082 S135082 (bases 8 to 1050, 7554 to 8506) Elango, N., Satake, M. and Venkatesan, S. MRNA sequence of three respiratory syncytial virus genes encoding two nonstructural proteins and a 22K structural protein J. Virol. 55 (1), 101-110 (1985)	85237684
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Collins,P.L., Dickens,L.B., Buckler-White,A., Olmsted,R.A., Spriggs,M.K., Camargo,B. and Coelingh,K.V. Nucleotide sequences for the gene junctions of human respiratory syncytial virus reveal distinctive features of intergenic structure
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Respiratory syncytial virus is a negative-strand RNA pleomorphic enveloped virus of the genus Pneumovirus. The matrix protein has no homology with the matrix proteins of other negative-stranded RNA viruses, implying that RS virus has undergone extensive evolutionary divergence. Two unidentified reading frames which potentially encode proteins were located: one overlaps the matrix protein and the other the F protein. The biological significance of these two reading frames is not clear. The positive strand is
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Collins, P.L. and Wertz, G.W.
Nucleotide sequences of the 1B and 1C nonstructural protein mRNAs
Of human respiratory syncytial virus
Virology 143 (2), 442-451 (1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      syncytial virus reveals an unusual type of viral membrane protein
Proc. Natl. Acad. Sci. U.S.A. 82 (12), 4075-4079 (1985)
85216636
                                                                                                                                                                                                                                                                             Satake, M., Coligan, J. E., Elango, N., Norrby, E. and Venkatesan, S. Respiratory syncytial virus envelope glycoprotein (G) has a novel
                                                                                                   Respiratory syncytial virus fusion glycoprotein: nucleotide sequence of mRNA, identification of clasavage activation site and amino acid sequence of N-terminus of F1 subunit Nucleic Acids Res. 13 (5), 1559-1574 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of the G protein gene of human respiratory
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7 (bases 5602 to 7423)
Elango,N., Satake,M., Coligan,J.E., Norrby,E., Camargo,E. and
Venkatesan,S.
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Wertz,G.W., Collins,P.L., Huang,Y., Gruber,C., Levine,S. and
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Collins, P.L. and Wertz, G.W.
The 1A protein gene of human respiratory syncytial virus:
nucleotide sequence of the mRNA and a related polycistronic
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Collins, P.L., Anderson, K., Langer, S.J. and Wertz, G.W.

Correct sequence for the major nucleocapsid protein mRNA or sepiratory syncytial virus
Virology 146 (1), 69-77 (1985)
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/organism="Human respiratory syncytial virus"
/strain="A2"

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Unclassified.
1 (bases 1 to 15222)
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2 Torrence,P.F., Silverman,R.Hugh., Cirino,N.Mario., Li,G. and Xiao,W.
RName L activators and antisense oligonuclectides effective treat RSV infections
Patent: Use 599860.2A 23 07-DEC-1999;
Location/Qualifiers Length 15222; ô Indels cch 92.8%; Score 853.4; DB 6; al Similarity 95.5%; Pred. No. 1.2e-177; 878; Conservative 0; Mismatches 41; 5401 8 6 AR093219 15222 bp I Sequence 23 from patent US 5998602. AR093219

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T. "Frame shift mutations as a novel mechanism for the generation of newtralization resistant mutants of human respiratory syncytial
T. "Perme shift mutations of human respiratory syncytial
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M. InterPro; IPR000925; Glycoprot_G.
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M. Prosize; PR00001; PHOSPHOPANTETHEINE; 1.
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sp_bhage:*
sp_plant:*
sp_rodent:*
sp_varus:*
sp_varus:*
sp_vartebrate:*
sp_unclassified:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
sp_mammal:*
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Query Match
Best Local Similarity 91.33
Matches 272; Conservative
                          01-JUL-1997 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. Attachment protein (G).
             01-JUL-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
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               181 TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKOLKPQTTKPKEVPTTKPTBEPTINTTK 240
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                                                                                                         241 TNITTILLINNTIGNPKLISQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 298
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                                                                                                                                                                                                                                                                                                                                                                                                             "Evolutionary pattern of human respiratory syncytial virus (subgroup A): cocirculating lineages and correlation of genetic and antigenic changes in the G glycoprotein.";

J. Virol. 68:548-5458(1994).

EMBL; Z33429; CAA83872.1; -.

InterPro; IPR000925; Glycoprote G.

InterPro; IPR000825; Ppantne attach.

PROSTIE; PS00082; Glycoprotein G; I.

PROSTIE: PS00082; Glycoprotein G; I.
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MEDLINE=54335057; PubMed=8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
Melero J.A.;
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                                                                                                                                                                                                                                                                        Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Glycoptotein (Fregment).
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Matches 295; Conservative
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Tolley K.P., Marriott A.C., Simpson A., Plows D.J., Matthews D.A., Longhurst S.J., Evans J.E., Johnson J.L., Cane P.A., Easton A.J., Pringle C.R.;
Pringle C.R.;
"Identification of mutations contributing to the reduced virulence a modified strain of respiratory syncytial virus.";
Vaccine 14:1637-1646(1956).
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Yiruses; sRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
VCBI_TaxID=11250;
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, 103662; AAC57026.1;
InterPro; IPR000925; Glycoprot G.
InterPro; IPR006162; Ppantne attach.
Pfam; PF00802; Glycoprotein G; PROSTE; PS001012; PROSTEDE PROSTICE; PS08012; BY08012; PROSTICE; PS08012; BY08012; PS08012; PS08012; PS08012; PS08018012; PS08018018; I.
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
04, Created)
04, Last sequence update)
23, Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Attachment glycoprotein (G).
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91.3%; Pred. No. 4.3e-95;
vative 7; Mismatches 19;
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Best Local Similarity
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MEDLINE=99022964; PubMed=9806017;
Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
T. "Antigenic and genetic diversity among the attachment proteins of
group A respiratory syncytial viruses that have caused repeat
to infections in children.";
J. Infect. Dis. 178.925-93.

R. EMBL; AF065405; AAD02941.1;
R. EMBL; AF065405; AAD02941.1;
R. InterPro; IPR006162; Pantne attach.
R. InterPro; IPR006162; Pantne attach.
R. Ffam; PP00802; Glycoprotein G; 1.
R. PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
                                                                                              "Idemification of mutations contributing to the reduced virulence of a modified strain of respiratory syncytial virus.";
Vaccine 14:1637-1646(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSKAKDORTAKTLEKTWDTLAHLLFISSGLYKLALKSVAQITLSILAMIISTSLITALI
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                         Tolley K.P., Marriott A.C., Simpson A., Plows D.J., Matthews D.A., Conghurst S.J., Evans J.B., Johnson J.L., Cane P.A., Easton A.J., Pringle C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.0%; Score 1389; DB 12; Length 298; 90.9%; Pred. No. 8.4e-95; ive 7; Mismatches 20; Indels 0;
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Baston A.J.;
Baston A.J.;
Baston A.J.;
Submitted (CCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U39661; AACS7036.1; -.
InterPro; IPR000325; Glycoprot G.
InterPro; IPR006162; Papatine attach.
Féan; PF00802; Glycoprotein G; 1.
FROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 298 AA; 32779 WW; 67F4A043682FA450 CRC64;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Human receiver.
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MEDLINE=97185152; PubMed=9032893;
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Best Local Similarity 90.9
Matches 271; Conservative
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                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                 1 MSKNKDORTAKTLERTWDTLNHLLFISSCLYKLNLKSVAQITLSILAMIISTSLIIAAII
                                                                                                                       61 FIASANHKVTLTTALIQDATSQIKOTTPTYLTQDPQLGISFSNLSELTSQTTTLLASTTP
                                                                                                                                                                                          121 GVKSNLOPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP
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                                                  1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4.9e-93;
ches 21;
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89.9%; Pred. No. 5.8e-93;
iive 10; Mismatches 20;
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                   Mismatches
 90.2%; Pred. No.
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Matches 267, Conservative
                     Conservative
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Best Local Similarity
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ESCUENCE FROM N.A.

STRAIN=Bubgroup A;

KEDLINE=9435057; PubMed=8057427;

MEDLINE=9435057; PubMed=8057427;

MEDLINE=9435057; PubMed=8057427;

A darcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J., Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,

Melero J.A.;

Melero J.A.;

Melero J.A.;

A): cool:culating lineages and correlation of genetic and antigenic changes in the G glycoprotein.";

A): cool:collating lineages and correlation of genetic and antigenic changes in the G glycoprotein.";

LU Virol. 68:5448-5455(1994).

EMBL; Z33422; CAA83875.1...

EMBL; Z33422; CAA83875.1...

RITE-Pro; IPR000925; Glycoprot G.

RITE-Pro; IPR000925; Glycoprotein G; Employer Greek G
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Matches 265, Conservative
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Q1-NOV-1996 (
Q1-NOV-1996 (
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          181 TCWAICKRIPNKKPGKRTTTKPTKKPTLKTTKKDPKPQTTKSKEVPTTKPTEEPTINTTK 240
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                                                          241 TNITTILLINNTIGNPKLISQMETPHSTSSEGNLSPSQVSTISEHPSQPSSPPNTTR 297
                                                                                       241 TNIITTLITSNITRNPELISQMETFHSTSSEGNPSPSQVSITSEYPSQPSSPPNTSR 297
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J. Infect. Dis. 178:925-932(1998).

EMBL, APG65406; AAD02942.1; -

InterPro; IPR006162; Ppantne attach.

Pram, PP008082; Glycoprot.

Fram, PP00802; Glycoprot.

PROSITE; PS00012; PH00FANTETHINE; 1.

SEQUENCE 298 AA; 32781 MW; AR7C9E05547C5745 CRC64;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
                                                                                                                                                                                                                                                                                                                                                                                        Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Attachment glycoprotein G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.8%; Score 1356; DB 12;
88.9%; Pred. No. 2.3e-92;
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Matches 265; Conservative 10; Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=WV5222;
MEDLINE=99022964; PubMed=9806017;
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                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                 RESULT 7
Q9YVB4
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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TNITTTPLTSNITTRNPELTSQMETFHSTSSEGNPSPSQFSITSEYPSQPSSPPNTSR 297
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                                                                                                                                     1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                       1 MSKNKOQRTAKTLERTWDTLAHFLESCLYKLANLKSVAQITLSILAMIISTSLIIAAII
                                                                       Gaps
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Changes in the G glycoprotein.";

While, 23428; CAA83871.1; -.

InterPro; IPR000925; Glycoprot_G.

InterPro; IPR00652; Ppantne attach.

PROSTES, PRO0012; PHOSPHORATETHEINE; 1.

SRQUENCE 297 AA; 32555 MM; 9D0A69BECAEGBGC8 CRC64;
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STRAIN=BUDGTOUP A;
STRAIN=B4335057, PubMed=8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
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87.7%; Score 1354; DB 12; Length 297;
89.2%; Pred. No. 3.2e-92;
ive 10; Mismatches 22; Indels 0;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
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INITITILINNITIGNPKLISOMETFHSISSEGNLSPSQVSITSEHPSQPSSPPNTTR 297
                                                                                                          TNITTILITNNTIGNPKLISQMBIFHSISSEGNLSPSQVSITSEHPSQPSSPPNTT 296
                                                                                                                                     1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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A and B Strains
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Attachment glycoprotein ( Fragment).
Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Last sequence update)
Last annotation update)
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88.2%; Pred. No. 4.1e-91;
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SEQUENCE FROM N.A.
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J. Virol. 68:5448-5459(1994).

EMBL; 233456; CAA83879.1; -.
InterPro; IPR0001925; Glycoprot G.
InterPro; IPR001025; Pantne attach.
PROM: Pfam; PR00802; Glycoprotein G;
PROM: ProsPHOPANTETHEINE; 1.
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88.5%; Pred. No. 1.7e-91;
ive 10; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-subgroup A;
MEDLINE-94335057; PubMed-8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.
Melero J.A.;
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Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
                                                                            Indels
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                           DB 12;
                                                                            23;
                     87.1%; Score 1345; DB 12
88.9%; Pred. No. 1.5e-91;
ive 10; Mismatches 23
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                                                                         264; Conservative
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les 262; Conservative
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                   Query Match
Best Local Similarity
Matches 264; Conserv
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01-MAR-2003
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295 AA;
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Matches 261; Conserv
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SEQUENCE FROM N.A.
NON TER
SEQUENCE
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                                                                                                           Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.,
"Antigenic and genetic diversity among the attachment proteins of
group A respiratory syncytial viruses that have caused repeat
infections in children."

J. Infect. Dis. 178:225-932(1998).

EMBL, AR065407; AAD02943.1; -.

Enterpro, IRR000925; Glycoprot G.

Interpro, IRR000162; Phantne attach.

Pfam; PR00802; Glycoprotein G; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
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Viruses; sBRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=12814;
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Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; X73353; CAA51764.1; -.
InterPro; IPR000125; Glycoprot_G.
InterPro; IPR00612; Panchre attach.
Pfam; Pf00802; Glycoprotein G; 1.
PROSITE; P800012; PHOSPHOPANTETHEINE; 1.
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Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment
subgroup A respiatory syncytial vuruses.";
J. Gen. Virol. 72:2091-2096(1991).
                                                                                                                                                                                                                                                                                                                                                                         293 AA; 32125 MW; 17B5B43396A63CCF CRC64;
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01-NOV-1996 (TrEMBirel. 01, Last sequence update)
01-NOV-2003 (TrEMBirel. 23, Last annotation update)
G protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
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Pred. No. 6.6e-91;
7; Mismatches 22
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                                                                       STRAIN=WV6973;
MEDLINE=99022964; PubMed=9806017;
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Best Local Similarity 90.1%;
Matches 264; Conservative
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                                               SEQUENCE FROM N.A.
    NCBI_TaxID=11250;
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MEDLINE=91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
Identification of variable domains of the attachment (G) protein subgroup A respiatory syncytial vuruses.";
J. Gen. Virol. 72:2091-2096(1991).
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Respiratory syncytial virus.
Viruses, BRNA negative-errand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                          Length
                                                                                                                           Indels
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Cane P.A.;
InterPro;
InterPro; IPR001925; Glycoprot G.
InterPro; IPR00162; Papatte attach.
Pfam; PF00802; Glycoprotein G; I.
PROSITE; PS00012; PHOSPHOPANTETHEINE; I.
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1 1
295 AA; 32490 MW; 48D835F670FF8006 CRC64;
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                                                                       DB 12;
                                                                    Query Match 86.4%; Score 1334; DB 12
Best Local Similarity 88.4%; Pred. No. 9.4e-91;
Matches 260; Conservative 8; Mismatches 26
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MEDLINE-Subgroup A;

MEDLINE-Subgroup A;

MEDLINE-Subgroup A;

MEDLINE-Subgroup A;

Melero J. Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,

Melero J.A.;

Melero J.A.;

Melero J.A.;

T. "Evolutionary pattern of human respiratory syncytial virus (subgroup A;

N. cocirculating lineages and correlation of genetic and antigenic A;

J. virol. 68:5448-545(1994).

MEMBL: Z33426; CAA83869.1; -.

MENEL: Z3426; CAA83869.1; -.

MINTEPPO; IPRO00025; Glycoprotein...

DR InterPro; IPRO0162; Papatne attach.

MENEL: S900012; PHOSPHOPANTETHEINE; 1.

SEQUENCE 298 AA; 32729 MW; 4E890FPD43845744 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Last sequence update)
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
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Search completed: October 29, 2003, 17:40:52 Job time : 75.283 sec8

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 29, 2003, 17:12:25; Search time 16.3057 Seconds (without alignments) 859.454 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-462-816-2 1544 1 MSKNKDQRTAKTLEKTWDTL.....VSTTSRHPSQPSSPPNTTRQ 298

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ф			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length	EG	QI	scription
1	1530	99.1	298	М	VGLG HRSVL	P20895 human respi
2	1418	91.8	298	Н	VGLG HRSVA	human
m	1343	87.0	297	Н	VGLG HRSV3	human
4	1343	87.0	297	Н	VGLG_HRSV6	human
ហ	1328	86.0	297	Н	VGLG_HRSV7	human
9	1324	82.8	297	Н	VGLG_HRSV4	human
7	1313	85.0	298	М	VGLG HRSV5	human
00	1307	84.7	297	н	VGLG HRSV2	human
σ,	767.5	49.7	292	Н	VGLG_HRSV8	human
10	761	49.3	292	٦	VGLG_HRSV1	human
11	309.5	20.0	263	н	VGLG_BRSV1	bovine
12	308.5	20.0	263	н	VGLG_BRSV4	bovine
13	299	19.4	257	н	VGLG_BRSVC	bovine
14	295.5	19.1	263	н	VGLG BRSV2	bovine
12	294.5	19.1	263	Н	VGLG_BRSVW	bovine
16	285	18.5	257	Н	VGLG_BRSVS	bovine
17	284	18.4	263	Н	VGLG_ORSVW	Q86695 ovine respi
18	279	18.1	257	Н	VGLG_BRSV7	bovin
13	270	17.5	257	7		bovine
50	267	17.3	257	-1	VGLG_BRSVR	Q84183 bovine resp
21	208	13.5	307	-	SGS3_DROME	_
22	198.5	12.9	2812	1		Q9y493 homo sapien
23	194	12.6	662	-1		
77 0	193	12.5	5179	н.		
57	191	12.4	1161	-	DAN4_YEAST	P47179 saccharomyc
56	183	11.9	217	-	SGS3_DROSI	-
7.7	171.5	•	2282	Н		P57999 oryctolagus
28	170	•	5703	Н	MUSB_HUMAN	Q9hc84 homo sapien
53	169.5	11.0	1367	-	AMYH_YEAST	
30	164.5	٠	2476	7	ZAN_PIG	Q28983 sus scrofa
H (6	S	10.4	263	Н	SGS3_DROYA	P13728 drosophila
21 c 20 c	159.5	10.3	907	П		
33		10.2	5376	7	ZAN_MOUSE	

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0; Gaps

Query Match Best Local Similarity 99.0%; Pred. No. 8.6e-93; Matches 295; Conservative 1; Mismatches 2; Indels

P28968 equine herp 007284 epstein-bar	P46590 candida alb Q09624 caenorhabdi	Q62635 rattus norv	Q01836 listeria in Q13854 schizosacch	F38594 BACCharomyc P39712 BACCharomyc P38739 BACCharomyc
VGLX_HSVEB VGP3_BBVA8	ALS1_CANAL YS89_CAEEL MIES HIDAN	MUC2_RAT CH12_COCPO	P60 LISIN YFGG SCHPO	YAG3_YEAST WSC4_YEAST
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156.5 155	155 155 154	150.5	146.5 146.5	144.5
34 35	37	30,04	4 4 4 1 2 c	44

ALIGNMENTS

PRT; 298 AA. ed) sequence update) annotation update) G (Attachment glycoprotein G).	Human respiratory syncytial virus (subgroup A / strain Long). Yiruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus. REST TAXID=11260; Ill SEQUENCE FROM N.A. WEDLINE-87289557; PubMed=2441388; Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.; MEDLINE-87289557; PubMed = 2441388; Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.; SEQUENCE FROM N.A. MEDLINE-87289557; PubMed=2441388; Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.; Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).	t_G. CYTOPLASMIC (POTENTIAL). POTENTIAL. EXTRACELLULAR (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL).
RESULT 1 VGLG HRSVL ID VGLG HRSVL STANDARD; LC P20855; DT 01-FEB-1991 (Rel. 37, Last sec DT 01-FEB-1996 (Rel. 33, Last sec DT 01-FEB-1996 (Rel. 33, Last ann DT 01-FEB-1996 (Rel. 34, Last ann DT 01-FEB-1996 (Rel. 34, Last ann DT 01-FEB-1996 (Rel. 34, Las	Nurses; serNA negative-strand viruse; Mononegavirales; Viruses; serNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus. [1] _TaxID=11260; [1] _TaxID=11260; [2] _TaxID=11260; [3] _SEQUENCE FROM N.A. MEDLINE=87288557; PubMed=2441388; "The G glycoprotein of human respiratory syncyrial virus subgroups A and B: extensive sequence divergence between antigenically related proteins."; Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987). -I FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT HENAGGLUTINATING ACTIVITIES. -I SUBSERANCE SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEU HENAGGLUTINATING ACTIVITIES. -I SUBSELLUAR LOCATION: EXPRESSED ON THE SURFACE OF THE CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRION. -I PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRADE DISTRIBUTED AMONG THE 91 SERINE AND THREGONINE RESIDU	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinfort the Buropean Bioinformatics Institutions as lon modified and this statement is not remove entities requires a license agreement (Sor send an email to license@isb-sib.ch).	EMBL; M17212; AAA47411.1; PIN, A32703; MGNZEL. InterPro; IPR000925; Glycoprot G. Pfam; PF00802; Glycoprotein. G; 1. Transmembrane; Glycoprotein. G; 1. TRANSMEM 67 298 EXTR. CARBOHYD 103 103 N-LII CARBOHYD 237 237 N-LII CARBOHYD 237 237 N-LII CARBOHYD 251 251 N-LII CARBOHYD 254 294 N-LII SEQUENCE 298 AA; 32781 MM; B7;
REES: VGL ID PT DT DT OB	\$	3888888888	S P P P P P P P P P P P P P P P P P P P

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SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95266253; PubMed=7747420; Connors M., Cover U.B. Jr., Firestone C.Y., Murphy B.R., Collins P.L.; A cold-passaged, attenuated strain of human respiratory syncytial virus contains mutations in the F and L genes.";
                        1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSIAQITLSILAMIISTSLITAII
MSKNKDQRTAKTLEKTWDTLNHLLF1SSGLYKLNLKSVAQ1TLS1LAM11STSL11TA11
                                                                                   FIASANHKVTLTTAIIQDATSQIKWTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-85216636; PubMed=385885; Wertz G.W. Levine S., Ball L.A.; Wertz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.; "Nucleotide sequence of the G protein gene of human respiratory syncytial virus reveals an unusual type of viral membrane protein."; Proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).
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passaged human respiratory syncytial virus vaccine candidate results
from the acquisition of a single mutation in the polymerase (L)
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Crowe J.E. Jr., Firestone C.Y., Whitehead S.S., Collins P.L.,
Murphy B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-86067198; PubMed-4069997;
Satake M., Coligan J.E., Elango N., Norrby E., Venkatesan S.;
"Respiratory syncytial virus envelope glycoprotein (G) has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human respiratory syncytial virus (strain A2).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virus Genes 13:269-273(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virology 208:478-484(1995)
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                          91.8%; Score 1418; DB 1; Length 298; 93.3%; Pred. No. 1.6e-85; ive 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ........ respiratory syncytial virus (strain rsb1734).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G.
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                                                                                                                                                 EMBL; X03149; CAA26928.1; -. EMBL; U50362; AA886653.1; -. EMBL; U50363; AA886653.1; -. EMBL; U63644; AAC55969.1; -.
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Best Local Similarity 88.5
Matches 262; Conservative
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CARBOHYD
CARBOHYD
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VGLG_HRSV7
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WEDDING PROM N.A.

WEDDING PAINT ACTION OF PLINGLE C.R.;

Cane P.A., Matthewa D.A., Pringle C.R.;

Cane P.A., Matthewa D.A., Pringle C.R.;

Cane P.A., Matthewa D.A., Pringle C.R.;

"Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";

"J. Gen. Virol. 7:2091-2096(1991).

"G. SEPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGATION ACTIVITIES.

"G. SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INPECTED C. SUBCELLULAR LOCATION: EXPRESSED ON THE MEMBRANE OF THE VIRIONS.

"G. SUBCELLULAR LOCATION: EXPRESSED ON THE MEMBRANE OF THE VIRIONS.

"DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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                                                                                                                                                                                                                                                                                                                                                   FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSBITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                                                     GVKSNLOPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVPNFVPCSICSNNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTBEPTINTTK 240
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                                                                                                                                                                                                                                                                                                               1 MSKNKDQRTAKTLERTWDTLANHLEFISSCLYKLNLKSVAQITLSILAMIISTSLIIVALI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNITILITUTIONPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPNTTR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
                                                                                                                                                                                                                                                                                               1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                        Gaps
HEMAGGLUTINATING ACTIVITIES.

-!- SUBGELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INPECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIKIONS.

-!- PTM: MAY CARRY 40-480 SEPRARTE O-LINKED CAREDCHURAR CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TNITTLITSNITRNPELTSOMETFHSTSSEGNPSPSQVSITSEYPSQPSSPPNPR
                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                         87.0%; Score 1343; DB 1; Length 297; 88.6%; Pred. No. 1.2e-80;
                                                                                                                                                                                                                                                                      23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus (strain rsb6256).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11256;
                                                                                                                                                                                                     251 N-LINKED (GLCNAC. . .) (Po
32525 MW; 48448F9E091E1802 CRC64;
                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                        ; Pred. No. 1.2e
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 AA
                                                                                                                                           POTENTIAL.
                                                                  PIR, JQ1205, JQ1205.
InterPro, IPR000925, Glycoprot G.
Pfam; PF00802, Glycoprotein G; I.
Transmembrane, Glycoprotein.
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InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                     Conservative
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297
135
237
251
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67
67
135
135
237
251
297 AA;
                                                                                                                                                                                                                                                      Local Similarity
les 263; Conserv
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VGLG HRSV6
ID VGLG HRSV6
P270Z5;
AUG-199;
                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                            1 MSKTKDQRTAKTLERTWDTLANHLLFISSCLYKLALKSIAQITLSILAMIISTSLIIAAII
                                                                                                                                                                                                                                                                                                                                                                                            61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQNPQLGISFSNLSETTSQPTTTPAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 INITITILINNTIGNPKITSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 296
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MEDLINE=91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment (G) protein of
EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                               Score 1343; DB 1; Length 297;
Pred. No. 1.2e-80;
8; Mismatches 26; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human respiratory syncytial virus (strain rsb6614).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
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61 FIASANHKVTLTTAIIQDATSQIKNTTQTVLTQNTQLGISFSNLSBTTSQPTTPPALTTP 120
                             1 MSKTKDQRTAKTLERTWDTLAHLLFISSCLYKLNLKSIAQITLSILAMISTSLIIAAII
                1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                 61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP
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InterPro. PR000925, Glycoprot G.
Pfam, PF00802; Glycoprotein G; 1.
Transmembrane; Glycoprotein.
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103
1135
237
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103
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298 AA;
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DOMAIN
CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
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VGLG_HRSV5
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                                                                                                                                                                                                                                                                           240
                                                                                                                                           61 FIASANHKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                     120
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                                                                                                                                                                                                                                                TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTK 240
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Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";
J. Gen. Virol. 72:2091-2096(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- FTM: MAX CARRY 40-80 SEBRARAE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                         61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQNPQLGISFSNLSETTSQPATTPALTTP
                                                                                                                                                                                                                                                                  181 TCWAICKRIPNKKPGKKTTTKPTKKPTIKTTKKOLKPQTTKPKEVLTTKPTEKPTINTTK
                                                                                                       1 MSKTKDQRTAKTLERTWDTLANHLLFISSCLYKLANLKSIAQITLSILAMIISTSLIIAAII
                                                                                         1 MSKNYDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITALI
                                                                                                                                                                                                                                                                                                   TNITTILITNNTTGNPKLISQMETFHSTSSEGNLSPSQVSTISEHPSQPSSPPNTT 296
                                                                                                                                                                                                                                                                                                                            TNIRITLLITTNITIGNPEYTSQKETLHSTSPEGNPSPSQVYTTSEYPSQPPSPSNTT 296
                                                                 Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL).
294 294 N-LINKED (GLCNAC. . .) (POTENTIAL) 297 AA; 32670 MW; 58B384028E437ACD CRC64;
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                                      Length 297;
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Pred. No. 2e-79;
7; Mismatches 29; Indels
                                                              29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human respiratory syncytial virus (strain rsb5857).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10488CCA475936BE CRC64;
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                                    86.0%; Score 1328; DB 1;
87.8%; Pred. No. 1.1e-79;
ative 7; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                             297 AA
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InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; I.
Transmembrane; Glycoprotein.
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                                                               Matches 260; Conservative
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294
297 AA;
                                                  Similarity
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Matches 260;
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P27023;
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                                      Query Match
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GVKSNLOPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                        TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEFPTINTTK 240
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1. Gen. Virol. 72:2091-2096(1991).

-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.

-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

-!- PTM: MAY CARRY 40-80 SERRARD O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                    181 TCWAICKRIPNKKPGKKTTTKPTKKPTIKTTKKDLKPQTTKPKEVLTTKPTEKPTINTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKTKDQRTAKTLEKTWDTLANFLEPISSCLYKLALKSIAQITLSILAMIISTSLIIAAII
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                                                                                                                                                                                                                                                                                                                           296
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                                                                                                                                                                                                                                                                                          241 TNIRTTLLTTWITGNDEYTSQKETLASTSPEGNPSPSQVYTTSEYPSQPPSPSNTT
                                                                                                                                                                                                                                                        THITTLITMNTTGNPKLTSOMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT
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N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
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%; Pred. No. 1.1e-78;
11; Mismatches 28; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus (strain rsb6190).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
VCBI_TaxID=11255;
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01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4D74E854D34D7BA5 CRC64;
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                                         SVESILGSTIVKTIKNTTITQIQPSKPTIKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                                                                           TCWAICKRIPSKKPGKKTTTKPTKKPTIKTTKCHKPQTTKPKBAPSTKPTEKPTINITK 240
                           GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                                                             TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTK 240
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PIASANNKVTLTTAIIQDATSQIKNTTPTYLTQNPQLGISFFNLSGTTSQTTAILALTTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHPEVFNFVPCSICSNNP 180
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                                                                                                                               241 TNITITILINNTIGNPKLISOMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTIRQ 298
                                                                                                                                            241 PNIRTTLLINSTTGNLEHTSQBETLHSTSSEGNTSPSQVYTTSEYLSQPISPSNITNQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                              subgroup A respiratory syncytial viruses...;
J. Gen. Virol. 72:2091-2096(1991).

-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTRINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTRIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- FTM: MAX CARRY 40-80 SEPRARE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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Viruses; ssRNa negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
                                                                                                                                                                                                                         297 AA.
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MEDLINE=91374005; PubMed=1895054;
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InterPro. IPR0000925, Glycoprot. G.
Pfam, PF00802; Glycoprotein. G; I.
Transmembrane; Glycoprotein.
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135
144
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DOMAIN
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TRANSMEM 38
DOMAIN 67
CARBOHYD 135
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WEDUINE-91374595; PubMed=1895391;
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WILLINE-91374595; PubMed=1895391;
WILLINE-91374595; PubMed=1895391;
WEDLINE-91374595; PubMed=1895391;
WILLINE-913745091;
WILLINE-913745091;
WILLINE-9137450919;
WILLINE-9137450919;
WILLINE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE THE AGGILTINATING ACTIVITIES.
C. I- PUNCTION: UNLIKE THE OTHER PRAMMINIDASE AND HEMAGGILTINATING ACTIVITIES.
C. I- SUBCELLUIRA AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
C. SUBCELLUIRA AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
C. I- SUBCELLUIRA AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
C. I- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
C. I- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
C. I- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sullender W.M., Anderson K., Wertz G.W.;
"The respiratory syncytial virus subgroup B attachment glycoprotein:
analysis of sequence, expression from a recombinant vector, and
evaluation as an immunogen against homologous and heterologous
subgroup virus challenge.";
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                                        241 TNIITTPLTSNTARNPELTSQMSTFHSTSSEGNPSPSQVSITSSYPPQPSSPPNTPR
241 INITITILITANTIGAPKLISOMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTR
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N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human respiratory syncytial virus (subgroup B / strain 8/60).
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                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI TaxID=11258;
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66 PC
292 E3
81 N-
100 N-
32143 MW;
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EMBL; M73545; AAA47408.1; -.
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                                                                                                                                                                                                                                                                                                        STANDARD;
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86
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292 AA;
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P23041;
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CARBOHYD
SEQUENCE
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TRANSMEM
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61 FILSANHKVTLTTVTVQTIKNHTEKNISTYLTQVPPERVNSSKQPTTTSPIHTNSATISP 120

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1 MSKHKNQRTARTLEKTWDTLNHLIVISSCLYRINLKSIAQIALSVLAMIISTSLIIAAII 61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 121 GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP

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                                                                               180
                                                                                                                                                            239
                                                                                                                                                                                 61 FIISANHKVTLTTVTVQTIKNHTGKNISTYLTQVPPERVNSSKQPTTTSPIHTNSATISP 120
                                                                                                                     121 NTKSETHHTTAQTKGRITTSTQTNKPSTKSRSKNPPKKPKDDYHFEVFNFVPCSICGNNQ 180
FIASANHKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSELTSQTTTLLASTTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87289657; PubMed=2441388;
Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
Johnson P.R., Striggs M.K., Olmsted R.A., Collins P.L.;
The G Blycoprotein of human respiratory syncytial viruses of
subgroups A and B: extensive sequence divergence between
antigenically related proteins.";
Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
-: FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                            TCWAICKRIPNKKPGKKTTTKPTKKPTPKTT-KKDLKPQTTKPKEVPTTKPTEEPTINTT
                                                                                 121 GVKSNLOPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP
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PTM: MAY CARRY 40-00 SEPARTE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                            240 KTNITTILITNNTTGNPKLISQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSP 292
                                                                                                                                                                                                                                                               241 ERDISTSQSTVIDITIPKYTIQQQSLHSTTSENTPSSTQIPTASE-PS-TSNP 291
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human respiratory syncytial virus (subgroup B / strain 18537). Viruses; ssNNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.3%; Score 761; DB 1; Length 292; 54.9%; Pred. No. 7e-43; ive 35; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1991 (Rel. 20, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@ib-sib.ch).
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FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE FUNCTION: UNLIKE THE OTHER PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.

SUBCELLULAR LOCATION: EXPRESSED ON THE SURPACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
                                      181 LCKSICKTIPSNKPKKKPTIKPTNKPTTKTTNKRDPKTPAKMPKKEIITNPAKKPTLKTT
181 TCWAICKRIPNKKPGKKTTTKPTKKPTFKTT-KKOLKPOTTKPKEVPTTKPTEEPTINTT
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MEDLINE=97288324; PubMed=9143302;
Furze J., Roberts S., Wertz G., Taylor G.;
"Antigenically distinct G glycoproteins of BRSV strains share a high degree of genetic homogeneity.";
virology 231:48-58(1997).
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N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                             240 KTNITTLLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPS 287
                                                                                                                                                                241 BRDTSISQSTVLDTITPKYTIQQQSLHSTTSENTPSSTQIPTASE-PS
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186 BY SIMILARITY.
187 BY SIMILARITY.
187 N-LINKED (GLCNAC. ...) (POTE 163 N-LINKED (GLCNAC. ...) (POTE 251 N-LINKED (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses, seRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sovine respiratory syncytial virus (strain 127)
                                                                                                                                                                                                                                                                                                                                                                                                15-UUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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263 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                              GVKSNLOPITVKTKNTTTTQTQPSK---PTTKQRQNKPPNKP-----NNDFH--FEVF 168
                                                                                                                                                                                                                                                                                                                                                                                                                   169 PHVPCSTCEGNPACSPLCQIELERAPSSAPTITLKKAPKPKTTKKPTKTTIYHRTSPEAK 228
                                                                                                                                                                                  61 YISVGNAKAKPISKPITQQIQUQHIPPPPLTEHNY------KSTHISIQSITL 108
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Furze J., Roberts S., Wertz G., Taylor G.;
Virology 231:48-58 (1997).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B HRS VIRUS.
                                  NFVPCSICSNNPTCWAIC----KRIPN-----KKPGKKTTTKPTKKPTFKTTKKDLK
   MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNIKSVAQITLSILAMIISTSLIITAII
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine respiratory syncytial virus (strain 4642) (BRS).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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N-LINKED (GLCNAC. .) (POT
W; D592D79EF8BE9535 CRC64;
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                                                                                                                                                              FIASANHKVTLITALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                           121 GVKSNLOPTTVKTKNTTTTQTQPSK---PTTKQRQNKPPNKP-----NNDFH--FEVF 168
                                                                                                                                                                                                    61 YISVGNAKAKPISKPITQQIQLQNHTPPPLIEHNY------KSTHTSIQSTIL 108
                                                                                                                                                                                                                                                                                   109 SOPPNIDITSGTTYGHPINRIONRKIKSOSTPLATRKPPINPLGSNPPENHQDHNNSOTL 168
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Biochemistry 35:14684-14688(1996).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
                                                                                                                  1 MSNHTHHPKFKTLKRAWKASKYFIVGLSCLYKFNLKSLVQTALTTLAMITLISLVITAII
                                                                                                                                                                                                                                                                                                                                                                169 PHVPCSTCEGNPACSPLCQIBLERAPSSAPTITLKKAPKPKTTKKPTKTTIYHRTSPEAK
                                                                                 1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                                                                          169 NFVPCSICSNNPTCWAIC----KRIPN-----KKPGKKTTTKPTKKPTFKTTKKDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91012801; PubMed=2214024;
Lerch R.A., Anderson K., Wertz G.W.;
Nucleotide sequence analysis and expression from recombinant vectors
demonstrate that the attachment protein G of bovine respiratory
syncytial virus is distinct from that of human respiratory syncytial
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
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SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECT CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doreleijers J.F., Langedijk J.P.M., Haard K., Boelens R., Rullmann J.A., Schaaper W.M., van Oirschot J.T., Kaptein R., "Solution structure of the immunodominant region of protein G
        Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BRS)
                                               Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine respiratory syncytial virus (strain Copenhagen) (Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                253
                                                                                                                                                                                                                                                                                                                                                                                                                                     229 LQTKKIMVTPQQGILSSP---EHQTNQSTTQISQHTS 262
    20.0%; Score 308.5; DB 1; 32.5%; Pred. No. 1.5e-13; ive 32; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                          217 PQTTKPKEVPTTKPTEEPTINTTKTNITTLTNNTT
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                         Conservative
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                      Similarity
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Query Match
Best Local Simil
Matches 90; (
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61 YISVGNAKAKPTSKPTIQOTQOPQNHTSPFFFFHNY-----KSTHTSIQSTTL 108
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(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine respiratory syncytial virus (strain 220-60) (BRS) Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                         28569 MW; OB86D541FBA0657D CRC64;
                                                                                                                                                  POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                 3D-structure.
CYTOPLASMIC (POTENTIAL)
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NCBI TaxID=82819;
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                                                                                                                                                                                                                                               N-LINKED
N-LINKED
N-LINKED
N-LINKED
                       PDB; 1BRV; 05-JUN-97.

InterPro; IPR000925; Glycoprot_G. Pfam; PF00802; Glycoprotein_G; 1.

POWALN 37 CYTO TRANSMEM 38 66 POTE
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                                                                                                                                                                                                                                                                                                                                                                                             180 1
257 AA;
PIR; A36408; MGNZBR
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SEQUENCE
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Best Local
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VGLG BRSV2
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  NA REPT TO THE TOTAL SOLUTION STATES AND STA
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-1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTIMATING ACTIVITIES.

-1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 ICSNNPTCWAIC----KRIPN-----KKPGKKTTTKPTKKPTFKTTKKDLKPOTTKP
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MEDDINE=9728124; PubMed=9143302;
Purze J., Roberts S., Wertz G., Taylor G.;
*Antigenically distinct G glycoproteins of BRSV strains share a high degree of genetic homogeneity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                            66 POTENTIAL.
263 EXTRACELLULAR (POTENTIAL).
186 BY SIMILARITY.
182 BY SIMILARITY.
127 N-LINKED (GLCNAC. ..) (POTE
163 N-LINKED (GLCNAC. ..) (POTE
251 N-LINKED (GLCNAC. ..) (POTE
251 N-LINKED (GLCNAC. ..) (POTE
251 N-LINKED (GLCNAC. ..) (POTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Major surface glycoprotein G (Attachment glycoprotein
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15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
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                                                                                                                                                                                                                                                                    HSSP; P22261; IBRV.
InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; I.
Transmembrane; Glycoprotein.
                                                                                                                                                                                                         EMBL; Y11205; CAA72089.1; -. PIR; JQ2284; JQ2284.
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176
127
163
163
251
263 AA;
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ID VGLG BRSVW
AC 010687;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.1%; Score 294.5; DB 1; Length 263; 30.8%; Pred. No. 1.2e-12; Live 35; Mismatches 102; Indels 63; Gaps
                                                                                                                                                                                                                                                                                     66 POTENTIAL.

263 EXTRACELLUIAR (POTENTIAL).

186 BY SIMILARITY.

182 BY SIMILARITY.

85 N-LINKED (GLCNAC. .) (POTENTIAL).

127 N-LINKED (GLCNAC. .) (POTENTIAL).

163 N-LINKED (GLCNAC. .) (POTENTIAL).

233 N-LINKED (GLCNAC. .) (POTENTIAL).

234 N-LINKED (GLCNAC. .) (POTENTIAL).

235 N-LINKED (GLCNAC. .) (POTENTIAL).

236050 MM; 0D06AF7FCB46B858 CRC64;
SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B HRS VIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 KITKKOLKPO----TIKPKEVPITKPIEEPIINTIKINITILLINNIT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                     EMBL; Y08717; CAA69967.1; -.
HSSP; P22261; IBRV.
InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; 1.
Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 30.8
                                                                                                                                                                                                                                                                                                                                                                                                                        263 AA;
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TRANSMEM
DOMAIN
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DISULFID
CARBOHYD
CARBOHYD
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CARBOHYD
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Search completed: October 29, 2003, 17:38:37 Job time : 18.3057 secs

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 29, 2003, 17:33:35; Search time 28.6755 Seconds (without alignments) 999.400 Million cell updates/sec Run on:

US-09-462-816-2

1 MSKNKDQRTAKTLEKTWDTL......vsTTSEHPSQPSSPPNTTRQ 298 Perfect score:

BLOSUM62 Sequence:

Scoring table:

283308 seqs, 96168682 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	1530	99.1	298	-	MGNZRI	major surface glyc
7	1418	91.8		-	MGNZ	major surface glyc
٣	1343	87.0	297	~	JQ1205	ment pro
4	1343	87.0		N	JQ1208	attachment protein
S	1333	86.3		7	JC5680	G protein - Human
9	1328	86.0		~	JQ1209	u
7	1324	85.8		~	JQ1206	
ω	1313	85.0		7	JQ1207	attachment protein
თ	1307	84.7		N	JQ1204	attachment protein
10	767.5	49.7		Н	MGNZ60	
11	761	49.3		Н	MGNZ18	major surface glyc
12	425	27.5		Н	VHNZ	
13	299	19.4	250	~	PQ0768	O
14	299	19.4	257	н	MGNZBR	major surface glyc
15	295.5	19.1	263	~	JQ2284	glycoprotein G - b
16	284	18.4	263	~	JQ2388	glycoprotein G - o
17	280	18.1	248	N	PQ0769	glycoprotein G - b
18	272	17.6	263	~	A48732	attachment glycopr
19	208	13.5	307	-	GSFF3	salivary glue prot
20	194	12.6		N	A45155	
21	193	12.5		N	A43932	mucin 2 precursor,
22	191	12.4		~	T22696	hypothetical prote
23	191	12.4		~	S57180	probable membrane
24	190	12.3		N	A53715	apomucin precursor
25	188	12.2		~	T31113	mucin-like glycopr
56	185.5	12.0	379	N	850125	larval glue protei
27	183	11.9		~	S01358	salivary glue prot
28	183	11.9	354	~	T46740	microfilarial shea
29	177	11.5	770	~	T22808	hypothetical prote

hypothetical prote promastigote surfa hypothetical prote	mucin - rhesus mac mucin SAC (clone J mucin MUC5B, trach	glucan 1,4-alpha-g hypothetical prote mucin, tracheal (A	ascites sialoglyco zonadhesin - pig promastigote surfa	mucin 5AC (clone J 171-7 protein - fr membrane glycoprot membrane glycoprot	
T29634 S20074 T34369	151920 853363 745025	S48478 E86185 A37232	A53577 T34022 S20075	S53362 S62335 T45462 T45463	
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320	34 33	34 38 38	2 4 4 0 4 1 1 1 0	4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	

ALIGNMENTS

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major surface glycoprotein G - human respiratory syncytial virus (strain Long)
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: A32703; S12279
R;Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Matl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and A;Reference number: A32703; MUID:87289657; PMID:2441388 A; Accession: A32703

A; Molecule type: mRNA.
A; Molecule type: mRNA.
A; Residues: 1-298 «JOH»
A; Residues: 1-298 «JOH»
A; Cross-references: GB:M17212; NID:g333940; PIDN:AAA47411.1; PID:g333941
A; Cross-references: GB:M17212; NID:g333940; PIDN:AAA47411.1; PID:g333941
B; Garcia-Barreno, B.; Portela, A.; Delgado, T.; Lopez, J.A.; Melero, J.A.
BY MED J. 9, 4181-4187, 1990
A; Mill: Frame shift mutations as a novel mechanism for the generation of neutralization A; Reference number: S12279; MUID:91065351; PMID:2249671
A; Residues: 1-298 «GAR»
A; Molecule type: mRNA
A; Residues: 1-298 «GAR»
C; Superfamily: respiratory syncytial virus major surface glycoprotein G
C; Keywords: glycoprotein; transmembrane protein
F; 41.63/Domain: transmembrane #status predicted <TMN>
F; 85,103,135,179,237,250,251,273,294/Binding site: carbohydrate (Asn) (covalent)

ô Gaps ; 0 99.1%; Score 1530; DB 1; Length 298; 99.0%; Pred. No. 2.3e-92; tive 1; Mismatches 2; Indels C Query Match Best Local Similarity 99.04 Matches 295; Conservative

1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSIAQITLSILAMIISTSLIITAII 60 1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII 60 g ð

61 PIASANHKVILTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSBITSQTTTILASTTP 120 61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120 ò

121 GVKSNLOPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180 121 GVKSNLQPTTVKTKNTTTQTQPSKPTTKQRQNKPPNKFNNDFHFEVPKVSCSICSNNP 180 ò 셤

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181 TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEBPTINTTK 240 181 TCMAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDHKPQTTKPKEVPTTKPTEEPTINTTK 240 ద ò

241 INITITILINNTTGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 298 241 TNIITTLITMITTGNPKLISQMETFHSTSSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 298 ठे

N RESULT

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Query Match 87.0%;
Best Local Similarity 88.6%;
Matches 263; Conservative 1:
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                                                                                                                                                                                                                                                                                  A;Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid protein A;Note: this protein may carry 40-80 separate 0-linked carbohydrate chains distributed a R;Satake, M.; Coligan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S. Nucleic Acids Res. 13, 7795-7812, 1985
A;Title: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure.
A;Reference number: A93599; MUID:86067198; PMID:4069997
                                                                                                                                                                                                                                                                   띵
                        C; Species: human respiratory syncytial virus
C; Species: human respiratory syncytial virus
C; Jozte: 28-May-1996 #sequence revision 28-May-1996 #text_change 24-Sep-1999
C; Accession: A94048; A93599; A04039
R; Wertz, G.W.; Collins, P.L.; Huang, Y.; Gruber, C.; Levine, S.; Ball, L.A.
Rxcc, Natl. Acad. Sci. US.A. 82, 4075-4079, 1985
A; Title: Nucleotide sequence of the G protein gene of human respiratory syncytial virus
A; Reference number: A94048; MUID: 85216636; PMID: 3858865
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C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-298 <WER>
A;Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217;
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A;Residues: 1-597 <CAN>
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory
ildren and adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, COSB-references: GB:X03149; NID:g60997; PIDN:CAA26928.1; PID:g60998
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;38-66/Domain: transmembrane #Ftus predicted <TNM>
F;38-66/Domain: transmembrane #Ftus predicted <TNM>
F;85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
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attachment protein - human respiratory syncytial virus (strain RSB1734)
NyAlternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSKNKDORTAKTLEKTWDTLAHLLFISSGLYKLALKSVAQITLSILAMIISTSLIITAII
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91.8%; Score 1418; DB 1; Length 298;
Best Local Similarity 93.3%; Pred. No. 4.2e-85;
Matches 278; Conservative 6; Mismatches 14; Indels
surface glycoprotein G - human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: JQ1205
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment A;Reference number: JQ1204; MUID:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: A93599
A, Molecule type: mRNA
A, Residues: 1-298 <SAT>
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C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
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NyAlternate names: G protein
C;Species: human respiratory syncytial virus
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1208 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1208 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
G;Accession: JQ1208 #sequence long for the attachment (G) protein of subgroup
A;Reference number: JQ1204; MUID:91374005; PMID:1895054
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A;Residues: 1-297 <CAN>
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
ildren and adults.
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      Length 297;
                                                          23; Indels
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; Score 1343; DB 2;
; Pred. No. 3.1e-80;
11; Mismatches 23;
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Pred. No. 3.1e-80;
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87.0%; Score 1343; D
Best Local Similarity 88.5%; Pred. No. 3.1e
Matches 262; Conservative 8; Mismatches
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C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predi
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R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A;Reference number: JQ1204; MUID:91374005; PMID:1895054
A;Accession: JQ1206
A;Molecule type: mRNA
A;Ressidues: 1-297 <CAN>
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CiDate: 31.Mar-1992 #sequence_revision 31.Mar-1992 #text_change 16-Feb-1997
CiAccession: J01207
RiCane, P.A.; Matthews, D.A.; Fringle, C.R.
G. Gene, P.A.; Matthews, D.A.; Pringle, C.R.
A. Gene, Virol. 72, 2031-2086, 11991
A. Title: Identification of variable domains of the attachment (G) protein of subgroup
A. Reference number: J01204; MUID:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C_iComment: Respiratory syncytial virus commonly causes severe lower respiratory tractildren and adults.
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                                                                                    121 GVKSNIQPTTVKTKNTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFUFVPCSICSNNP 180
                                                                                                                         TCWAICKRIPNKKPGKKTTTKPTKKPTPKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTK 240
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                  61 FIASANHKWTLTTAIIQDATSQIKMTTPTYLTQNPQLGISFSNLSETTSQPATTPALTTP 120
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NiAlternate names: G protein
CiSpecies: human respiratory syncytial virus
CiSpecies: Jumar_1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
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N;Alternate names: G protein
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87.8%; Pred. No. 5.3e-79;
tive 7; Mismatches 29;
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Matches 260; Conservative
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A;Molecule type: mRNA
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G protein - Human respiratory syncytial virus
C;Species: Human respiratory syncytial virus
C;Species: Human respiratory syncytial virus
C;Date: 11.Nov-1997 #sequence_revision 11.Nov-1997 #text_change 26-Feb-1998
C;Accession: UC5680
C;Accession: UC5680
C;Accession: UC5680
A;Title: Molecular analysis of G protein gene of a respiratory syncytial virus strain is
A;Reference number: UC5680
A;Reference number: UC5680
A;Rolecule type: mRNA
A;Residues: 1-298 CGEN>
A;Residues: 1-298 CGEN>
A;Residues: 1-298 CGEN>
A;Residues: 1-298 CGEN>
A;Roctimental source: strain B79
A;Note: the authors translated the codon TTT for residue 165 and 170 as Glu, TTC for res
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
F;1-38/Domain: intracellular #status predicted <INT>
F;39-66/Domain: extracellular #status predicted <INT>
F;67-298/Domain: extracellular #status predicted <INT>
F;67-298/Domain: extracellular #status predicted <INT>
F;67-298/Domain: extracellular #status predicted <INTO>
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N.Alternate names: G protein

N.Alternate names: G protein

C.Species: human respiratory syncytial virus

C.Species: human respiratory syncytial virus

C.Accession: J01209

R.Cane, P.A.; Matthews, D.A.; Pringle, C.R.

J. Gen. virol. 72, 2091-2096, 1991

A.Title: Identification of variable domains of the attachment (G) protein of subgroup A A.Title: Identification of variable domains of the attachment (G) protein of subgroup A A.Molecule type: mRNA

C.Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il comment: Respiratory syncytial virus major surface glycoprotein G

C.Seywords: glycoprotein; transmembrane protein

F.85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
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                       22.
                                                                   C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
P;85,103,135,237,250,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subgroup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 PNIRTTLLTNSTIGNLEHTSQEETLHSTSSEGNTSPSQVYTTSEYLSQPTSPSNITNQ 298
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31-Mar-1992 #text_change 16-Feb-1997
                                                                                                                                                                                                                                   1 MSKTKDQRTAKTLEKTWDTLNHLLFISSCLYKLNLKSIAQITLSILAMISTSLIIAAII
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                                                                                                                                        85.0%; Score 1313; DB 2; Length 298; larity 86.9%; Pred. No. 2.7e-78; Conservative 11; Mismatches 28; Indels
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86.5%; Pred. No. 6.7e-78;
ive 12; Mismatches 28; Indels (
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C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_chang
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_chang
C; Accession: JQ1204
B; Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72 2091-2096, 1991
A; Title: Identification of variable domains of the attachment
A; Reference number: JQ1204; MUID:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     attachment protein - human respiratory syncytial virus N;Alternate names: G protein
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                                                                                                                                                       Similarity
A;Residues: 1-298 <CAN>
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A, Molecule type: mRNA
A, Residues: 1-297 <CAN>
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hes 259;
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Best Local S:
Matches 259
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Best Local S:
Matches 257,
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major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)
N;Alternate names: attachment glycoprotein G
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: A37077
K;Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A;Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis of gous subgroup virus challenge.
A;Reference number: A37077; MUID:90357765; PMID:1697126
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(Species: human respiratory syncytial virus
(Species: human respiratory syncytial virus
(Spate: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
(Spacession: B3270)
(Spacession: B3270)
(Spate: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
(Spacession: B3270)
(Spate: 31-Mar-1991)
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A;Molecule type: mENA
A;Residues: 1-292 <SUL>
A;Kesidues: 1-292 <SUL>
C;Genetics: EMBL:M55633; NID:G333944; PIDN:AAA47413.1; PID:g333945
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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: MSA
A.Molecule type: MSA
A.Fesidues: 1-29 c.00H
A.Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
C.Superfamily: respiratory syncytial virus major surface glycoprotein G
C.Keywords: glycoprotein; transmembrane protein
F;41-63/Domain: transmembrane #status predicted TMNA
                                                     241 TNIITTPLTSNTARNPELTSQMETFHSTSSEGNPSPSQVSITSEYPPQPSSPPNTPR
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49.7%; Score 767.5; DB 1; Length 292;
Best Local Similarity 55.3%; Pred. No. 6.4e-43;
Matches 162; Conservative 34; Mismatches 94; Indels 3
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es 94; Indels
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Nillernate names: attachment glycoprotein G
Cispecias: bounds tespiratory syncytial virus
Cidate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
CiAccession: A36408
Fileron, R.A.; Anderson, K.; Wertz, G.W.
J. Virol. 64, 5559-5569, 1990
A;Title: Nucleotide sequence analysis and expression from recombinant vectors demonst)
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CiKeywords: glycoprotein; transmembrane protein
Fy45-62/Domain: transmembrane #status predicted <TMN>
Fy45-82,127,149,233,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;60-250/Domain: extracellular #status predicted <BXT>
F;78,156,226,241,244/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         major surface glycoprotein G - bovine respiratory syncytial virus (strain 391-2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 GTTYGHSTDETQSRKIKSQSTLPTTRKPPINPSESNPPENHQDHNNSQTLPYVPCSTCEG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 NPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKOLKPOTTKPKEVPTTKPTEEPTINT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 TKTNITITILINNTTGNPKLISQMETPHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----HHRTSPEAKLOPKN-NTAAPOOGILSSPENHTNO 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GVKSNLQPTTVKTKNTTTTQTQPSK---PTTKQRQNKPPNKPNNDF-------HFEVF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 SQLLNIDTTRGITYGHSTNETQNRKIKGQSTLPATRKPPINPSGSIPPENHQDHNNFQTL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 NFVPCSICSNNPTCWALCKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 PYVPCSTCEGNLACLSLCH------IETERAPSRAPTI-TLKKTPKPKTTK------ 212
                                                                                                                                                                                                                                                                                                                                                                                                                               71 LTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSBITSQTTTILASTTPGVKSNLQPTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 KTLEKTWDTLNHLLFISSGLYKLNIKSVAQITLSILAMIISTSLIITAIIFIASANHKVT 70
                                                                                                                                                                                                                                                                                                                     4 KTLKRAWKASKYFIVGLSCLYKFNLKSLVQTALSTLAMITLTSLVITAIIYISVGNAKAK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 NLACLSLCQVGPGR------APSRAPTI-TLKKTPKPKTTK------KP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 KPTEEPTINTTKTNITTLLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQV 279
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                                                                                                                  DB 2; Length 250;
                                                                                                          y syncytial virus.
A;Reference number: A36408; MUID:91012801; PMID:2214024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>-</del>
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A; Residues: 1-257 <LER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: A36408
                                                                                                                  Query Match
Best Local Si
Matches 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleocapsid protein (version 2) - human respiratory syncytial virus
C; Species: human respiratory syncytial virus
C; Date: 25-Reb-1985 #sequence_revision 25-Reb-1985 #text_change 16-Jul-1999
C; Accession: A04026
R; Elango, N:; Venkatesan, S.
Nucleic Acids Res: 11, 5941-5951, 1983
A; Title: Amino acid sequence of respiratory syncytial virus capsid protein.
A; Reference number: A04026
A; Molecule type: mRNA
A; Residues: 1-467 < ELA>
A; Cross-references: GB:X00001; NID:g61215; PIDN:CAA24906.1; PID:g61216
C; Generics:
A; Gene: N
C; Superfamily: respiratory syncytial virus nucleocapsid protein
C; Keywords: nucleocapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 TLKTTKKDPKPQTTKSKEVPTKPTEEPTINTTKTNIITTLTSNTTGNPELTSOMETFH 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 TFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTTLLTNNTTGNPKLTSQMETFH 266
                                                                                                                                                                                                                                                                             61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                                  61 FIISANHKVTLTTVTVQIIKNHTEKNISTYLTÖVPPERVNSSKOPTTSPIHTNSATISP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCWAICKRIPNKKPGKKTTTKPTKKPTFKTT-KKDLKPQTTKPKEVPTTKPTEBPTINTT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                   GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
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                                                                                                                      1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                   1 MSKHKNORTARTLEKTWDTLNHLIVISSCLYRLNLKSIAQIALSVLAMIISTSLIIAAII
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                                                2; Gaps
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A,Molecule type: mRNA
A,Residues: 1-250 «MA.
C,Superfamily: respiratory syncytial virus major surface glycoprotein G
C,Reywords: glycoprotein; transmembrane protein
F;1-31/Domain: intracellular #status predicted <INT>
F;32-59/Domain: transmembrane #status predicted <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 BRDTSISOSTVLDTITPKYTIQQQSLHSTTSENTPSSTQIPTASE-PS 287
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        ; Fred. No. 1.7e-42;
35; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 STSSEGNPSPSQVSTTSEYPSQPSSPPNTPRQ 467
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        54.98;
                                            Matches 158; Conservative
        Best Local Similarity
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Jycoprotein G - bovine respiratory syncytial virus (isolate A51908)
C;Species: bovine respiratory syncytial virus
C;Species: 14-011-1994 #sequence_revision 14-011-1994 #text_change 07-May-1999
C;Accession: J02284
R;Mallipeddi, S.K.; Samal, S.K.
J. Gen. Virol. 74, 2001-2004, 1993
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial vA;Reference number: J02284; MUID: 93389461; PMID: 8376974
A;Reference number: J02284; MUID: 93389461; PMID: 8376974
A;Reference number: J02284; MUID: 93389461; PMID: 8376974
A;Reference number: J02284; MUID: 93899461; PMID: 8376974
A;Reference number: J02284; MUID: 93899461; PMID: 8376974
C;Superimental source: isolate A51908
C;Superimental source: isolate A51908
C;Superimental source: scalar status predicted <CTMA:
F;39-66/Domain: intransmembrane #status predicted <CTMA:
F;39-66/Domain: extracellular #status predicted <EXT>
F;27-263/Domain: extracellular #status predicted <EXT>
F;127,163,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FIASANHKVTLITALIQDATSQIKNTTPTYLTQDPQLGISFSNLSELTSQTTTILASTTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 GTTYGHPINRTÖNRKIKSGSTPLATRKLPINPL----ESNPPENHQDHNNSQTLPHVPCS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 ICSNNPTCWAIC----KRIPN-----KKPGKKTTTKPTKKPTFKTTKKDLKPQTTKP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 TCEGNPACSPLCQIGLERAPSRAPTITLKKAPKPTTTTYHRTSPEAKLQTKKN 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.1%; Score 295.5; DB 2; Length 263;
Best Local Similarity 31.7%; Pred. No. 2.3e-12;
Matches 86; Conservative 35; Mismatches 123; Indels 27; Gaps
213 KPTK--TTIHHRTSPETKLQPKNNTATP----QQGILSSTEHHTNQSTTQI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 KEVPITKPIEEPIINTIKINITILLINNIT 253
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Job time : 31.6755 secs
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GenCore version 5.1.6
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October 29, 2003, 17:41:00 ; Search time 52.2906 Seconds (without alignments) 975.349 Million cell updates/sec OM protein - protein search, using sw model Run on:

1 MSKNKDQRTAKTLEXTWDTL.......VSTTSEHPSQPSSPPNTTRQ 298 US-09-462-816-2 1544 Perfect score:

BLOSUM62 Scoring table: Sequence:

642050 seqs, 171146064 residues Searched:

Gapop 10.0 , Gapext 0.5

642050 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/ptodata/1/pubpaa/PCT_RBW_PUB.pep:*
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6: \cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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11: \cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
13: \cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
14: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
15: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
16: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
16: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
17: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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18: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
18: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Query Match Length DB	DB	ID	Description	
-	193	12.5	;	6	US-09-922-217-1068	Sequence 1068, Ap	
7	193	12.5	۳.	10	US-09-833-263-1068	Sequence 1068, Ap	
m	193	12.5	5179	14	US-10-025-380-1068	Sequence 1068, Ap	
4	177.5	11.5		12	US-10-029-386-32198	Sequence 32198, A	
ß	169.5	11.0	•	10	US-09-801-368-108	Sequence 108, App	
y	169	10.9		12	US-10-351-641-871	Sequence 871, App	
7	162.5	10.5	288	Q	US-09-216-393-341	Sequence 341, App	
æ	162.5	10.5		σ	US-09-216-393-344	Sequence 344, App	
6	162.5	10.5		12	US-10-321-856-341	Sequence 341, App	
10	162.5	10.5		12	US-10-321-856-344	Sequence 344, App	
11	162	10.5		14	US-10-124-557-14	Sequence 14, Appl	
12	162	10.5	_	14	US-10-124-557-84	Sequence 84, Appl	
13	162	10.5	-1	14	US-10-124-557-74	Sequence 74, Appl	
14	162	10.5		14	US-10-124-557-58	28,	
15	162	10.5	-	14	US-10-124-557-104	104,	

Sequence 44, Appl Sequence 42, Appl Sequence 50, Appl Sequence 60, Appl Sequence 60, Appl Sequence 41, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 110, Appl Sequence 110, Appl Sequence 110, Appl Sequence 21, Appl Sequence 224,
4 US-10-124-557-44 4 US-10-124-557-42 4 US-10-124-557-142 4 US-10-124-557-146 4 US-10-124-557-46 4 US-10-124-557-40 4 US-10-124-557-40 4 US-10-124-557-40 4 US-10-124-557-52 4 US-10-124-557-52 5 US-10-124-557-62 5 US-10-124-557-62 6 US-10-124-557-62 7 US-10-124-557-62 8 US-10-124-557-62 9 US-10-124-557-62 1 US-09-804-348 1 US-09-804-348 1 US-09-801-368-110 1 US-09-801-368-110 1 US-09-901-630-21 2 US-10-301-822-49 2 US-10-301-822-49 2 US-10-176-847-54 5 US-10-176-847-54 5 US-10-140-011-224 2 US-10-140-274-224 2 US-10-140-274-224 2 US-10-140-274-224 2 US-10-140-877-224
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162 162 162 162 162 162 162 162 162 162
11112222222222222222222222222222222222

ALIGNMENTS

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71 LITALIQDA - TSQIKNTTP----TYLIQDPQLGISFSNLSELT--SQTTTLLASTTPG 121
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Best Local Similarity 30.6%; Pred. No. 2.3e-06;
Matches 77; Conservative 23; Mismatches 114; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Clapper, Jonathan D. TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.471C13 CURRENT APPLICATION WUMBER: US/09/922,217 CURRENT FILING DATE: 2001-08-03 NUMBER: PSEQ ID NOS: 1124 SOFTWARE: FASSEG for Windows Version 4.0 SEQ ID NO 1068 LENGTH: 5179
               Sequence 1068, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
                                                                                                         APPLICANT: Xu, Jiangchun
APPLICANT: Su, Jiangchun
APPLICANT: Secriet, Heather
APPLICANT: Secriet, Heather
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Mang, Tongtong
APPLICANT: Stolk, John A.
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-922-217-1068
JS-09-922-217-1068
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Sequence 32198, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: ASONICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32198
LENGTH: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1624 TPI--TPPTSTTTLPPT----TTPSPPPTTTTPPPTTTPSPPTTTPSPPTTTTTTP 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 FEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.5%; Score 193; DB 14; Length 5179; Best Local Similarity 30.6%; Pred. No. 2.3e-06; Matches 77; Conservative 23; Mismatches 114; Indels 38;
                                                                                                                                                                                     APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
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ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: MAP TO ACCO7663.28
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 1129
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
        Madeleine Joy
                                                                                 Jiang, Yuqiu
Smith, Carole L.
King, Gordon E.
Wang, Aijun
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Meagher, Madelei
Stolk, John A.
Wang, Tongtong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-10-025-380-1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-10-029-386-32198
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 1068, Application US/09833263

Patent No. US20020110547A1

GENERAL INFORMATION:

APPLICANT: Ward, Aliun

APPLICANT: Clapper, John A.

APPLICANT: Stolk, John A.

APPLICANT: Maddleine J.

TITLE OF INVENTION: DIAGNOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOUNDS FOR COLON CANCER AND METHODS FOR THRIR USE

FILE REFERENCE: 210121.471C12

CURRENT APPLICATION NUMBER: US/09/833,263

CURRENT APPLING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 5179
                                                  1564 PPPTTTTTPPPPTTTTPSPPTTTTTPPPPTTTTPSPPTTTTPSPPTTTPSPPTT 1623
                                                                                                                                                         1624 TPI--TPPTSTTTLPPT-----TTPSPPTTTTPPPPTTTPSPPTTTPSPPTTTPT 1675
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                                                                                                          165 FEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKB 224
                                                                                                                                                                                                                    225 VPTTKPTEEPTINTTKTNITTLLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSE 284
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     -----QTQPSKPTTKQRQNKPPNKPNNDFH 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
12.5%; Score 193; DB 10; Length 5179;
Best Local Similarity 30.6%; Pred. No. 2.3e-06;
Matches 77; Conservative 23; Mismatches 114; Indels 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-10-025-380-1068
; Sequence 1068, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
  ----VKSNLQPTTVKTKNTTTT
                                                                                                                                                                                                                                                                                                                                                                                1732 SPTTTPSPPTTT 1743
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CRGANISM: Homo sapiens
US-09-833-263-1068
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140 QTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTT 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.9%; Score 169; DB 12; Best Local Similarity 94.4%; Pred. No. 3.5e-07; Matches 34; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSI 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                               Sequence 871, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION WURBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                              RESULT 6
US-10-351-641-871
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FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 KWTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGV--KSNLQPTTVKTKNTTT--T 139
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                                                                                                                                                                                                                                                                                                                                                                                                         129 TTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKR 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 IPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTT---KPTEEPTINTTKTNI-- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 บรราชการประชาบารประชาชาบารบารบารบารบารบารบารบารบารบารบารบาร
                                                                                                                                                                                                                                9 TAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAIIFIASANHK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 -TTTLLTNNTTGNPKLTSQMBTFHSTSSBGNLSPSQVSTTSEHPSQPSSPP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.0%; Score 169.5; DB 10; Length 1367; 26.2%; Pred. No. 3.5e-05; tive 36; Mismatches 94; Indels 45;
                                                                                                                                                                                   35;
                                                                                                                                   11.5%; Score 177.5; DB 12; Length 800; 23.7%; Pred. No. 3.9e-06; tive 39; Mismatches 148; Indels 35;
  OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. US20020128250Alman, Thea
Royer, John
Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 Tritistrrrrrrrrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 108, Application US/09801368 Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62; Conservative
                                                                                                                                                             Best Local Similarity 23.7% Matches 69; Conservative
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Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Summers, Eric
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Milne, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                          ; OTHER INFURMALLY
US-10-029-386-32198
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LENGTH: 1367
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APPLICANT:
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                                                                                                                                          Query Match
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; Sequence 341, Application US/09216393
; Patent No. US20010014447A1
; Batent No. US20010014447A1
; GENERAL INFORMATION:
; APPLICANT: Midhaush GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
; TITLE OF INVENTION: USES THEREOF
; TILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393
; CURRENT APPLICATION NUMBER: US/994,825
; RARLIER PILING DATE: 1998-12-18
; SAFLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 341
LENGTH: 288
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269 KEKPTPPTTTSCTKEKPTPPHHD-----TTPCT------KKKTTTSKTCTKKT 310
                                                                                                                    311 TTPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAP 370
                                                                                    200 TKPTKKPTFKTTKKDLKP-----QTTKPKBVPTTKPTEB-----PTINTTKTNITTL 247
                                                                                                                                                                                                                                               248 LINNITIGNPKLISQMETFHSTSSEGNLSPSQVSTTSEHPSQP-----SSPPNTT 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, M.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: LAMBORION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
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Patent No. US20010014447A1

GENERAL INCPEMENTION

TITLE OF INVENTION: TOXOPLASMA GONDI PROTEINS, NUCLEIC ACID MOLECULES, AND

TITLE OF INVENTION: TOXOPLASMA GONDI PROTEINS, NUCLEIC ACID MOLECULES, AND

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

CURRENT APPLICATION NUMBER: US/09/216,393

CURRENT FILING DATE: 1998-12-18

REARLIER FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 364

SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                   TTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVPNFVPCSICSNNPTCWAICKRIPNKKPG 195
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10.5%; Score 162.5; DB 9; Length 288; 23.1%; Pred. No. 1.8e-05; Live 22; Mismatches 99; Indels 95
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Best Local Similarity 23.1%; Pred. No. 1.8e-05;
Matches 65; Conservative 22; Mismatches 99; Indels 95
                                                                            39 AQITLSILAMIISTSLIITAIIFIASANHKVTLTTAIIQDATSQI---
                                                                                                                                                                                                                                                                                                                                                                             PKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 296
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CRGANISM: Toxoplasma gondii
US-09-216-393-344
                   Best Local Similarity 23.19
Matches 65; Conservative
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LENGTH: 288
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 Query Match
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RESULT

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APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
TITLE REPERRENCE: TX-1-C2-1
CURRENT APPLICATION NUMBER: US/10/321,856
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR PILING DATE: 1998-12-19
PRIOR PILING DATE: 1999-12-19
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PACHOLIN VERSION 3.1
SEQ ID NO 341
LENGTH: 288
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TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
FILE REPERBENCE: TX.-1-C2.1
CURRENT APPLICATION NUMBER: US/10/321,856
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR PILING DATE: 1999-12-19
PRIOR FILING DATE: 1999-12-19
PRIOR FILING DATE: 1999-12-19
RIOR PILING DATE: 1997-12-19
SEQ ID NOS: 366
SOFTWARE: PACENTION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
SEQ ID NO 344
LENGTH: 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Best Local Similarity 23.1%; Pred. No. 1.8e-05;
Matches 65; Conservative 22; Mismatches 99; Indels 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 10.5%; Score 162.5; DB 12; Length I Similarity 23.1%; Pred. No. 1.8e-05; 65; Conservative 22; Mismatches 99; Indels
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Sequence 341, Application US/10321856; Publication No. US20030194393A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 344, Application US/10321856; Publication No. US20030194393A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Toxoplasma gondii
US-10-321-856-341
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Best Local Similarity
Matches 65; Conserv
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US-10-321-856-344
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RESULT 12
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136 TTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKPG 195
                                                                                                                                                                                     196 KKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTLLINNTTGN 255
                                                                                                                                                                                                                                                                   84 -----KNTTPTYLTQDPQLGISFSNLSEITSQTTTTILASTTPGVKSNLQPTTVKTKN 135
                                                                                                      Jacobs, Kenneth
Hewick, Rodney M.
Hewick, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                         256 PKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 296
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION AUMBER: US 07/643,502
PILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
PILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1889
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1889
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-124-557-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-10-124-557-14
Sequence 14, Application US/10124557
Fublication No. US20020137894A1
GENERAL INFORMATION:
CENERAL INFORMATION:
CAPPLICANT: Turner, Katherine
CAPPLICANT: Calark, Stephen C.
Clark, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                  125 TSKVLAKPIPKAETITK-----GPALTTPKEPIPTIPKEPÄŠTIP---KEPTPITI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                        132 K-----TKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 NPTCWAICKRIPN-----KKPGKKTTTKP--------TKKPTFKTTK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 APTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTTPTPKEPAPTTKEPAPTTPK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 KDL----KPQTTKPKEVPTTKP-----TEEPTINTTKTNITTLLINNTTGNPKLTS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | 
                                                                                                                     Gaps
                                                                                                               78;
           DB 14; Length 941;
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Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
10.5%; Score 162; DB 14; Length 94
24.6%; Pred. No. 9e-05;
tive 26; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 TTKSAPTTPKE----PSPTTTKEPAPTTPKEPAPTT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18.7AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1889
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 84, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 84:
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                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                             Similarity
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                                                                                                               68;
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     Query Match
Best Local Si
Matches 68;
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TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
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US-10-124-557-58
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                                                                                                                                                                                                                                                                        132 K------TKNTTTTQTQPSKPTTKQRQNKPNNKPNNDFHFEVFNFVPCSICSN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 422
                                                                                                                                                                                       72 TTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV 131
                                                                                                                                                                                                                              206 İSKVLAKPİPKAETİİK-----ĞPALITPKEPİPTİPKEPASİİP---KEPTPİTI 253
                                                                                                                                                                                                                                                                                                                 -----APTTTKEP 302
                                                                                                                                                                                                                                                                                                                                                             ----TKKPTFKTTK
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                                                                                                                                                    Gaps
                                                                                                                                                  78;
                                                                                                      DB 14; Length 1022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 74, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney W.
Gennet, Thomas G.
TITLE OF INVENTION: Negakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                      10.5%; Score 162; DB 14; Length 1
24.6%; Pred. No. 0.0001;
tive 26; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                 254 KSAPTTPKEPAPTTİKSAPİTPKEPAPTİTKEPAPTTPKEP
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STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                           179 NPTCWAICKRIPN-----KKPGKKTTTKP---
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APPLICATION NUMBER: US 07/643,502
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 84: US-10-124-557-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
                                                                                   Query Match
Best Local Similarity 24.00.
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US-10-124-557-74
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                                                                                                                                                                                                                                                                                                                                                                                                                     132 K------TKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSN
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                                                                                                                                                                                                                                                                            72 TTAIIQDATSQIXNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 NPICWAICKRIPN-----KKPGKKTTTTKP-------TKKPTFKTTTK
                                                                                                                                                                                                                               78;
                                                                                                                                                                                  Length 1038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                        Query Match

10.5%; Score 162; DB 14; Length 1

Best Local Similarity 24.6%; Pred. No. 0.0001;

Matches 68; Conservative 26; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 296
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APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      74:
                            ; TOPOLOGY: Inhear MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-124-557-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 58, Application US/10124557
Publication No. US2020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
LENGTH: 1038 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02140
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 NPTCWAICKRIPN-----KKPGKKTTTKP-------TKKPTFKTTK 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDL-----KPQTIKPKEVPTIKP-----TEEPTINTIKTNITTLLINNTIGNPKLTS 260
                                                                                                                                                                                                                                                                                                                                                           78;
                                                                                                                                                                                                                                                                                                            10.5%; Score 162; DB 14; Length 1049; 24.6%; Pred. No. 0.0001; tive 26; Mismatches 104; Indels 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450 TTKSAPTTPKE----PSPTTTKEPAPTTPKEPAPTT 481
NAME: CSETT, LUADIN
REGISTRATION NUMBER: 31,822
REBERBRICH FLOCKER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-UAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-124-557-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 104, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <Unknown>
                                                                                                                        INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1049 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                        68; Conservative
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-10-124-557-104
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.5%; Score 162; DB 14;
24.6%; Pred. No. 0.00012;
APPLICATION NUMBER: US 07/457,196
                   FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                              5190
                                                                                                                                                                                                                                                                                                                 TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 NPTCWAICKRIPN-----KKPGKKTTTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: October 29, 2003, 17:54:26 Job time : 54.2906 secs
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: CSert. Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                             INFORMATION FOR SEQ 1D NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 24.6
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Sequence 12, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 27, Appli
Sequence 17, Appli
Sequence 27, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
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                                                                      October 29, 2003, 17:36:05; Search time 16.3057 Seconds (without alignments) 773.267 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, A Sequence 8, A Sequence 8, A Sequence 8, A Sequence 8, A Sequence 8, A Sequence 8, A Sequence 8, A Sequence 8, A Sequence 13, Sequence 13,
                                                                                                                                                1 MSKNKDQRTAKTLEKTWDTL......VSTTSEHPSQPSSPPNTTRQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8
Sequence 8
Sequence 2
                                                                                                                                                                                                                                                                                                                                                               1: /cgn2_6/ptcdata/2/jaa/5A COMB.pep:*
2: /cgn2_6/ptcdata/2/jaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/jaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/jaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/jaa/FCTUS COMB.pep:*
6: /cgn2_6/ptcdata/2/jaa/FCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-831-189D-8

US-08-344-639E-8

US-08-344-639E-8

US-08-467-961A-8

US-08-467-961A-8

US-08-467-961A-8

US-08-193-792-12

US-08-793-792-12

US-08-793-792-8

US-08-793-792-8

US-08-928-361B-8

US-09-588-995A-8

US-09-588-995A-5

US-09-588-995A-6

US-09-588-995A-6

US-09-588-995A-6

US-09-588-995A-6

US-09-588-995A-6

US-09-588-995A-6

US-09-588-995A-6

US-09-588-995A-6

US-08-928-361B-27

US-08-928-361B-27

US-08-928-361B-27

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US-08-928-361B-27

US-08-928-361B-27

US-08-928-361B-27

US-09-88-995A-27

US-09-88-995A-20

US-09-88-995B-27

US-09-88-871

US-09-88-871

US-09-88-871
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                               328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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188
187.5
187.5
187.5
183.5
173.5
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15444
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193
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                                                                                                                                                    Sequence:
                                                                          Run on:
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Sequence 341, App Sequence 344, App Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 104, Appl Sequence 104, Appl Sequence 104, Appl Sequence 142, Appl Sequence 60, Appl Sequence 60, Appl Sequence 60, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl	NCODING A CONFERS PROTECTION AGAINST RESPIRATORY SYNCYTIAL VIRUS
288 4 US-09-216-3938-341 288 4 US-09-216-3938-344 941 4 US-07-757-0228-14 1028 4 US-07-757-0228-84 1049 4 US-07-757-0228-84 11240 4 US-07-757-0228-42 11210 4 US-07-757-0228-42 11311 4 US-07-757-0228-42 1313 4 US-07-757-0228-46 1320 4 US-07-757-0228-46 1320 4 US-07-757-0228-46 1320 4 US-07-757-0228-46 1354 4 US-07-757-0228-46 1354 4 US-07-757-0228-40 1363 4 US-07-757-0228-40 1364 4 US-07-757-0228-40 1364 4 US-07-757-0228-40 1404 4 US-07-757-0228-40	MENTS ID GENE E IN WHICH C IRUS AND Version #
28 162.5 10.5 29 162.5 10.5 30 162.5 10.5 31 162.10.5 32 33 162 10.5 34 162 10.5 35 40 162 10.5 40 162 10.5 44 162 10.5 45 162	RESULT 1 US-08-467-963C-8 Sequence 8, Application US/08467963C PRECENT NO. 5968706 PRECENT NO. 5968706 PRECENT NO. 5968706 TITLE OF INVENTION: MULTIMERIC PROTEIT TITLE OF INVENTION: CHIMERIC PROTEIT TITLE OF INVENTION: CHIMERIC PROTEIT TITLE OF INVENTION: CHIMERIC PROTEITY: TOWNERSPRONDENCE ADDRESS: 38 CORRESPONDENCE ADDRESS: 38 CORPUTER: OR SEQUENCES: 38 COMPUTER: OR PROMING COMPATION: COUNTRY: Canada ZIP: MGG IR? COUNTRY: Canada ZIP: MGG IR? COMPUTER: TEMP C COMPATION: COUNTRY: CANADA CONDUTER: DEM PC COMPATION: MEDIUM TYPE: Floppy disk COMPUTER: PAPELICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/467,963; FILING DATE: 16-APR-1997 PRIOR APPLICATION NUMBER: US/08/467,963; FILING DATE: 06-JAN-1992 ATTORNEY APPLICATION NUMBER: US/08/401,554 FILING DATE: 06-JAN-1993 PRIOR APPLICATION NUMBER: 24,973 PRIOR APPLICATION NUMBER: 24,973 PRIOR APPLICATION NUMBER: 24,973 TELEFAX: (416) 595-1163 INPORMATION POR SEG ID NO: 8: SEGUENCE CHARACTERISTICS: LENGTH: 298 amino acids TELENTAL STEAMENTERISTICS: LENGTH: 298 amino acids STRANBENESS: single TOPOLOGY: linear

```
REFERENCE/DOCKET NUMBER: 1038-688 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08852344D Patent No. 6017539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                           Query Match
Best Local Similarity 100.
Matches 298; Conservative
JS-08-838-189D-8
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US-08-852-344D-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08838189D
Sequence 8, Application US/08838189D
Sequence 8, Application US/08838189D
GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: WIN-Pan
APPLICANT: DV, Run-Pan
APPLICANT: BWASYSHYN, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUBNZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Geh Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                     GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                   TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TCWAICKRIPNKKPGKKTTTKPTKRPTFKTTKKDLKPOTTKPKEVPTTKPTEEPTINTTK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THITTILINNITGNPKLISQMETFHSTSSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 298
                                                                                                                                                         1 MSKNKDQRTAKTLEKTWDTLMHLLFISSGLYKLNLKSVAQITLSILAMIISTSLITAII
                                                                                                                     1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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                    100.0%; Score 1544; DB 2; Length 298; 100.0%; Pred. No. 2.1e-132;
                                                                       Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRAIION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-687 MIS;jb
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                  0; Mismatches
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 595-115
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                        Local Similarity 100.
hes 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Ontario
COUNTRY: Canada
ZIP: MSG IRT
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-08-838-189D-8
                    Query Match
Best Local S
Matches 298
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121 GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFVFVFCSICSNNP 180
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                                                                                                                                                 1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                  Gaps
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APPLICANT: KLEIN, Michel H
APPLICANT: DU, Kun-Pan
APPLICANT: DU, Kun-Pan
APPLICANT: WASYEN: Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 377
CORRESPONDENCE ADDRESS:
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   Length 298;
                                                                              Indels
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STREET: Gth Floor, 330 University Avenue
CTIY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MGG 117
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PEN PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRAITHOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRAITHOS DATE: 07-MAY-1997
CLASSIFICATION NUMBER: US/08/852,344D
FILING DATE: 07-MAY-1997
CLASSIFICATION NUMBER: US 08/344,639
FILING DATE: 14-MOV-1994
PRICH APPLICATION NUMBER: GB 9200117.1
PRICH APPLICATION NUMBER: GB 9200117.1
PRILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
PREPERENTATION NUMBER: 24,039
PRICH APPLICATION NUMBER: BB 9200117.1
REGISTRATION NUMBER: 24,039
PRICH APPLICATION NUMBER: 24,039
PRICH APPLICATION NUMBER: 1040404
PREPERENTATION NUMBER: 24,030
PREPERENTATION NUMBER: 24,030
PREPERENTATION NUMBER: 24,030
PREPERENTATION NUMBER: 24,030
100.0%; Score 1544; DB 2;
100.0%; Pred. No. 2.1e-132;
tive 0; Mismatches 0;
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                                                                                                                                                                                                   1 MSKNKDQRTAKTLEKTWDTLAHLIFISSGLYKLNIKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                      1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                           Gaps
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                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-132;
Matches 298; Conservative 0; Mismatches 0; Indels 0
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APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Bwasyshyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: TOTONICO
CITY: TOTONICO
COUTRY: Canada
ZIP: MAG IR/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,639E
FILING DATE: 14-NOV-1994
CLASSITCATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSITCATION NUMBER: GB 9200117.1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 424
FILING DATE: 06-JAN-1992
CLASSIFICATION: 424
FILING DATE: 06-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
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NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-391 MIS
TELECOMMUNICATION INFORMATION:
TELEBHONE: (416) 595-1163
TELEX: 065-24667 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08344639E
Patent No. 6033668
; TOPOLOGY: linear
US-08-852-344D-8
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US-08-344-639E-8
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61 FIASANHKVTITTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
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COUNTER: CREATED
COUNTER: CREATED
COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATE:
APPLICATION NUMBER: US/08/467,969A
FLING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/01,554
FLING DATE: 06-JN-1993
CLASSIFICATION NUMBER: US 08/001,554
FLING DATE: 06-JAN-1993
CLASSIFICATION NUMBER: QS 200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: A35
ATORNEY/AGENT INPORMATION:
NAME: STEWARY, MACHAEL I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-475 MIS:bh
TELESPHONE: (416) 595-1155
                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-132;
Matches 298; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08467969A; Sequence 8, Application US/08467969A; Patent No. 6168786; GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
STREET: Toronto
STATE: Oncario
COUNTRY: Canada
ZIP. W. .
                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                        298 amino acids
SEQUENCE CHARACTERISTICS
                                                                      single
                                           TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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Best Local Similarity 100.0%; Pred. No. 2.1e-132;
Matches 298; Conservative 0; Mismatches 0; Indels 0
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COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMILIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,961A
FILING DATE: 06-JUN-1995
CLASSIFICATION BATA:
APPLICATION NUMBER: US 08/001,554
FILING APPLICATION 1435
RIOR APPLICATION 1435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 08/001,554
PRING APPLICATION NUMBER: US 08/001,554
PRING APPLICATION NUMBER: US 08/001,554
PRING APPLICATION NUMBER: US 08/001,554
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FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
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REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-08-467-969A-8
TELEFAX: (416) 595-1163
TELEK: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTORNEY/AGENT INFORMATION:
                                                                                                                                                      LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
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61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTEBPTINTTK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKNKDQRTAKTLEKTWDTLAHLLFISSGLYKLANLKSYAQITLSILAMIISTSLITAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKINLKSVAQITLSILAMIISTSLIITAII
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CONTRY: Canada
ZIP: MAGI IX
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,554A
FILING DATE: 06-JAN-1993
CURSSIFICATION: APPLICATION: APPLICATION APPLICATION APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION
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100.0%; Pred. No. 2.1e-132;
ive 0; Mismatches 0;
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Betent No. 6225091

GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Bwasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INPORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEFONE (416) 595-1155
TELEFAX: (416) 595-1155
TELEFAX: 065-24567 SIMBAS
                              TELECOMMUNICATION INFORMATION
TELEPRAM: (416) 595-1153
TELEPRAM: (416) 595-1163
TELERA: (646) 595-1163
TELERA: 065-24567 SINBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-467-961A-8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 298; Conservative
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Best Local Similarity
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us-09-462-816-2.rai

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 QLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            490 QLGISPSNPSEITSQITTILASTTPGVKSTLQSTTVKTKNTTTTQTQPSKPTTKQRQNKP 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 PNKPNNDFHFEVFNFVPCSICSNNPTCWAJCKRIPNKKPGKKTTTKPTKKPTFKTTKKDL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610 KPQTTKSKEVPTTKPTEEPTINTTKTNIITTLLISNTTGNPELTSQMETFHSTSSEGNPS 669
                                                                                                                                                                                                                                                                                                                                                                                                               61 FIASANHKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                       61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSBITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                                                                            121 GVKSNLOPTTVKTKNTTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTBEPTINTTK 240
                                                                                                                                                                                                                                          1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII 60
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                                                                                                                                                                   Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WATHEN, MICHAEL W.
TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING
JIMMUNOGENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY
                                                                                                                                                                                                      Indels
                                                                                                                                             100.0%; Score 1544; DB 3; Similarity 100.0%; Pred. No. 2.1e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNCYTLE, VIRUS

CURRENT APPLICATION DATA;

CURRINT APPLICATION DATA;

FILING DATE: 31-0CT-1988

PRIOR APPLICATION DATE:

PRIOR APPLICATION DATE:

PRIOR DATE: 31-0CT-1988

FILING DATE: 23-DEC-1987
                                   LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 PSQVSTTSE 284
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                                                                                          linear
                                                                                                          MOLECULE TYPE:
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                                                                                            TOPOLOGY:
                                                                                                                                                                                                        298;
                                                                                                                              US-08-001-554A-8
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Best Local &
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5194595-19
;Patent No.
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61 PIASANHKVTLĮTALIQDATSQIKNTĮPIYLĮQDPQLGISFSNLSELTSQTTTĮLASĮTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 GITYGHPINRTÖNRKIKSQSTPLATRKLPINPL----ESNPPENHQDHNNSQTLPHVPCS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 ICSNNPTCWAIC----KRIPN-----KKPGKKTTTKPTKKPTFKTTKKDLKPQTTKP 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Gaps
                                                            APPLICANT: Samal, Siba K
TITLE OF INVENTION: Bovine Respiratory Syncytial Virus Genes
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.1%; Score 295.5; DB 5; Length 263; 31.7%; Pred. No. 4.1e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: INVENTION: Antigenic peptides derived from the
                                                                                                                                                                  ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08177
FILING DATE: 19911104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 TATPQQGILSSP---EHQTNQSTTQISQHTS 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20509-96711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19911104
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/608,937
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION:
                    Sequence 13, Application PC/TUS9108177 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08793792; Patent No. 6077511; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Highet, David W
REGISTRATION NUMBER: 30,265
REFRENCE/DOCKET NUMBER: 2050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4854
TELEPHONE: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELBFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein PCT-US91-08177-13
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                20005
                                                                                                                                                                                                                      CITY: Wash
STATE: DC
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PCT-US91-08177-13
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                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 189
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Patent No. 6514697
GENERAL INPORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: NELSON, RICHARD C.
APPLICANT: NELSON, RICHARD C.
APPLICANT: WITH OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES OF THE STATE CONTINUES O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 TLITALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPT
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12.2%; Score 188; DB 3; Length 216
Best Local Similarity 26.4%; Pred. No. 1.8e-09;
Matches 60; Conservative 23; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
                                    APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES,
TITLE OF INVENTION: THERR FUNCTIONAL MUTANTS
TITLE OF INVENTION: FOR TREATMENT AND DETECT
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verry, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 irririririririri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 8:
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LENGTH: 216 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650-324-1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
          GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-928-361B-8
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                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.

NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.4%; Score 222; DB 3; Length 37; llarity 100.0%; Pred. No. 1.3e-13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.5%; Score 193; DB 3; Length 32; Best Local Similarity 100.0%; Pred. No. 4.5e-11; Matches 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 NKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 193
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                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: 02/08/793,792 FILING DATE:
                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 8, Application US/08928361B; Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acid TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-793-792-12
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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## APPLICANT: PETERSEN, CAROLYN
## APPLICANT: PETERSEN, CAROLYN
## APPLICANT: BARNES, DEBRA A.
## APPLICANT: BARNES, DEBRA A.
## APPLICANT: BARNES, DEBRA A.
## APPLICANT: MEANUS, DEBRA A.
## APPLICANT: MEANUS, DEBRA A.
## APPLICANT: MEANUS, DEBRA A.
## TITLE OF INVENTION: INFECTION OF CRYPTOSPORIDIUM
## TITLE OF INVENTION: INFECTIONS
## TITLE OF INVENTION: INFECTIONS
## TITLE OF INVENTION: INFECTIONS
## TITLE OF INVENTION: INFECTIONS
## TITLE OF INVENTION: INFECTIONS
## TITLE OF INVENTION OF CRYPTOSPORIDIUM
## TILING DATE: 1997-09-12
## PRIOR APPLICATION NUMBER: 08/927,171
## PRIOR APPLICATION NUMBER: 08/928,361
## PRIOR APPLICATION NUMBER: 08/700,651
## PRIOR APPLICATION NUMBER: 08/115,751
## PRIOR APPLICATION NUMBER: 08/115,751
## PRIOR APPLICATION NUMBER: 08/115,751
## PRIOR APPLICATION NUMBER: 08/115,751
## PRIOR APPLICATION NUMBER: 08/115,751
## PRIOR APPLICATION NUMBER: 08/115,751
## PRIOR APPLICATION NUMBER: 08/115,751
## PRIOR PRIING DATE: 1995-04-03
## PRIOR PRIING DATE: 1995-04-03
## PRIOR PRIING DATE: 1995-04-03
## PRIOR PRIING PATE: 1995-04-03
## PRIOR PRIUNG PATE: 1995-04-03
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## PRIOR PATE: 1995-04-03
## PRIOR PATE: 1995-04-03
## PRIOR PAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 IFDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTTTTTTTTT------TTTTTT 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 FNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 TKPTEEPTINTTKTNITTTLINNTTGNPKLTSOMETFHSTSSEGNLSPSOVSTTSEHPS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.2%; Score 188; DB 3; Length 1837; 22.7%; Pred. No. 3.5e-08; Live 32; Mismatches 161; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIIST---
                                                REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION 550-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09588995A Patent No. 6514697
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ORGANISM: Cryptosporidium parvum
                                                                                                                                                                                                                                                                                    1837 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.2%
Best Local Similarity 22.7%
Matches 70; Conservative

    MOLECULE TYPE: protein
US-08-928-361B-5
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STRANDEDNESS:
TOPOLOGY: linear
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US-09-588-995A-5
                                                                                                                                                                                                                                                                                    LENGTH:
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Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PERTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 TLITALIQDAISQIKNITPTYLIQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTLLT 249
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TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
FRIOR APPLICATION NUMBER: 08/827,171
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 12.2%; Score 188; DB 4; Length 216;
1 Similarity 26.4%; Pred. No. 1.8e-09;
60; Conservative 23; Mismatches 120; Indels 24;
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ZIP: 94206-1840
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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TYPE: PRT
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US-09-588-995A-5

Search completed: October 29, 2003, 17:42:22 Job time: 17.3057 secs

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Run on:

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PIV; RSV; multimeric; hybrid; pathogen; chimeric protein; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multimeric hybrid genes and their chimeric proteins - are vaccines against multiple pathogenic infections e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Respiratory syncitial virus (RSV) G protein.
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                                                                           AAR95616
AAR97050
AAY44078
AAB18805
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AAB84123
AAB68016
AAB67775
AAC22577
AAR985661
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AAR44080
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ABP97861
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 Respiratory syncitial virus
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N-PSDB; AAQ45686
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13-JAN-1994
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AAR39286;
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 Sequence of human
HSRV glycoprotein
HRSV glycoprotein
Respiratory syncyt
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695.249 Million cell updates/sec
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A Geneseg 1900n03:

SIDS1/gcgdata/geneseg/genesegp-embl/AA1980.DAT:*

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                                                                                                                         MSKNKDQRTAKTLEKTWDTL.....VSTTSEHPSQPSSPPNTTRQ 298
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          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                        1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAW96313
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                                                                              A novel multimeric hybrid gene is used as a vaccine. The gene consists of two gene sequences which are linked and encode antigenic regions, these two sequences being derived from two different pathogens (parainfluenza vitus (PIV) and respiratory syncitial vitus (RSV)). The gene sequences that are particularly used are those which encode PIV-3 F and MN proteins (AAQ45683, AAQ45684) and RSV F and (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TNITITLITNNTIGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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                                                                                                                                                                                                                                                                                                                          100.0%; Score 1544; DB 14; Length 298; llarity 100.0%; Pred. No. 2.6e-113; Conservative 0; Mismatches 0; Indels 0;
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para-influenza virus and respiratory syncytial virus
                                        Claim 11; Figure 7A-7D; 80pp; English.
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ses 298; Conserv
                                                                                                                                                                                                                                                                                  298 AA;
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                                                                                                                                                                                 vaccines by inserting the trivers which into a non-replicating vector. The G protein is placed under the control of alternative signal and expression sequences, for example the chimeric G protein produced may also comprise the signal peptide of tissue plasminogen activator (tPA). The recombinant vector may also comprise sequences upstream of the G protein gene which enhance the G proteins immunoprotective ability. The resulting immunogenic composition will agenerate antibodies directed against the RSV G protein when administered to a host organism. The composition is useful as a vaccine to immunise against RSV-associated disease, particularly resulting in a balanced Thl/Th2 immune response and for raising Ab, by usual immunisation and cell fusion methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
useful in protective vaccines and
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G protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1544; DB 20; Length 298; 100.0%; Pred. No. 2.6e-113; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                         respiratory syncytial virus (RSV) G protein can be
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                                 to raise antibodies for diagnosis
                                                                                          Claim 4; Fig 2; 67pp; English.
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(first entry)
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WPI; 1998-144802/13
  N-PSDB; AAQ29623
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                                                                                        A novel plasmid which comprises a DNA sequence encoding this protein, and the protein itself, are claimed, for use as HRSV vaccines. The vaccine can be administered to pregnant women or to women of child bearing age to stimulate maternal antibodies. Infants can also be vaccinated at 2-3 months of age. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine, human respiratory syncytial virus, HRSV, F; G; 22K; 9.5K;
                             Vaccines for human respiratory virus - comprising proteins or fragment encoded by a DNA sequence coding for human respiratory
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                                                                                                                                                                                    Match 91.8%; Score 1418; DB 8; Length 298; Local Similarity 93.3%; Pred. No. 2e-103; Heb 278; Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                                          14; Indels
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                                                                     Disclosure, Chart 13; 57pp; English.
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88US-0218737.
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                                                   syncytial virus proteins.
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WPI; 1987-206300/29
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          N-PSDB; AAN70784.
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13-JUL-1988;
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03-MAR-1993
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                                                                                                                                             The sequences of mRNA encoding HRSV structural proteins are given in AAQ28622-26. The proteins are F, G, 22K, 9.5K and major capsid protein N. The sequences and encoded proteins are useful for preparing vaccines against HRSV. The vaccines can be used to confer immunity against respiratory tract infections on human subjects. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Vaccines for human respiratory virus - include structural genes coding for native structural viral proteins and immunogenic fragments
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Pred. No. 2e-103;
6; Mismatches 14; Indels 0
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                                                                                               Disclosure; Page 18; 21pp; English
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86US-0818740.
86WO-US02756.
92US-0897171.
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93.3%;
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Best Local Similarity 93.3
Matches 278; Conservative
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                                                                                                                                                                                                                                  1 MSKNKDQRTAKTLERTWDTLNHLLFISSCLYKLNLKSVAQITLSILAMIISTSLIIAAII
                                                                                                                                                                                                                     1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                  Gaps
                    v
                  Production of human respiratory syncytial virus glyco-protein F or (
- by culturing eukaryotic host cells transfected with corresponding
                                                                              The present sequence was used in the development of a novel method for the production of human respiratory syncytial virus (HRSV) glycoprotein G (GpG). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV gpF or gpG. The gp can be used to prepare
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0
                                                                                                                                                                             DB 19; Length 298;
                                                                                                                                                                            Score 1418; DB 19; Length
Pred. No. 2e-103;
6; Mismatches 14; Indels
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                                                             Example 1; Columns 27-28; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Respiratory syncytial virus G protein.
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                                                                                                                                                                             91.8%;
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                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takimoto T;
                                                                                                                                      vaccines against HRSV.
                                                                                                                                                                                       Similarity
                                                                                                                                                        298 AA;
N-PSDB; AAV18736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200192548-A2
                                                                                                                                                                             Mac
Local S.
278;
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                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU74676;
                                                                                                                                                          Sequence
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                                                                                                                                                                             Query Match
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The invention relates to a recombinant Sendai virus comprising an exogenous nucleic acid encoding a paramyxovirus (PMV) protein or its antigenic fragment. The virus may be administered in combination with an antiviral chemotherapeutic compound. Two or more viruses expressing different PMV proteins nay be co-administered. Compositions comprising the virus are useful for eliciting a humoral and/or cellular immune response to a PMV in a mammal, particularly a human. Further a recombinant Sendai virus comprising an exogenous nucleic acid encoding a second PMV protein is also administered and priming and/or boosting humoral or cellular immune response comprises administering one or more of a recombinant or isolated PMV protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendai viral effective vaccine against PPIV or RSV (the major causes of paediatric effective vaccine against PPIV or RSV (the major causes of paediatric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVKSTLQSTTVKTKNTTTTQTQPSKPTTKQRQNKPPSKPNNDFHFEVFNFVFCSICSNNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TCWAICKRIPWKKPGKKTTTKPTKKPTLKTTKKDPKPQTTKSKEVPTTKPTEEPTINTTK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THITTLITSNITGNPELISQMETFHSTSSEGNPSPSQVSTISEYPSQPSSPPNTPRQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSKNKDQRTAKTLERTWDTLAHLLFISSCLYKLANLKSYAQITLSILAMIISTSLIIAAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FIASANHKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory disease) and also to express any gene of interest in target cells, providing a positive medical impact on impaired cells. Wild-type globin gene transfer (i.e. gene therapy) into stem cells effects a cure for sickle cell disease or betathalassaemia. The recombinant virus may also prove effective in conferring immunity to human immunodeficiency virus (HIV) infection. The Sendai virus replicates at level that is high enough to induce sufficient immunity, but does not cause any harm to human recipient. The presents equence represents a respiratory synoylial virus (RSV) G protein (heavily glycosylated protein), a PMV protein quitable for expression by the recombinant virus of the invention.
                                                                                                                      ģ
                                                                                                              Recombinant Sendai virus useful in vaccines to protect infection paramyxoviruses, comprises exogenous nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted G protein of respiratory syncytial virus
                                                                                                                                                                                                paramyxovirus protein or its antigenic fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                              Disclosure; Page 48; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW96314 standard; Protein; 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 278; Conservative
WPI; 2002-130534/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                        N-PSDB; AAS21045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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ID AAW
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G protein; respiratory syncytial virus; RSV; recombinant vector;

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216 KPQTIKPKEVPTTKPTEEPTINTTKTNITTTLLINNTTGNPKLISQMETFHSTSSEGNLS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          490 QLGISPSNPSEITSQITTILASTTPGVKSTLQSTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 PNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKPGKKTTTKPTKKPTFKTTKKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           610 KPQTIKSKEVPTIKPTEBPINITIKINIITILLISNITIGNPBLISQMETFHSISSEGNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 QLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory synctial virus; RSV; G-protein; annexin II; L-selectin; RSV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric polypeptide contg. a signal sequence and one or more immunogenic fragments from both human respiratory syncytial virus glycoproteins F and G. Can be used in vaccines. Hosts are, eg E. coli, Chinese hamster ovary cells, murine C127 cells and
      Chimeric human respiratory synctial virus glycoproteins F and
                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric human respiratory syncytial virus polypeptides(s) - contg. immunogenic fragments from HRSV glycoproteins F and G, for vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                          Chimeric polypeptide; human respiratory syncytial virus; protein F; protein G; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 901; DB 10;
Pred. No. 2.1e-62;
6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of RSV G-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; page 47-48; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB68336 standard; protein; 299 AA.
                                                                                                     Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.4%;
                                                                                                                                                                                                                                                             87US-0137387.
                                                                                                                                                                                                                      88WO-US03784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 91.0 es 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSQVSTTSE 284
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                                                                                                                                                                                                                                                                                               NHOPAN ( oran)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. frugiperda.
                                                                                                                                                                                                                                                             23-DEC-1987;
                                                                                                                                           WO8905823-A
                                                                                                                                                                                29-JUN-1989
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                                                                                                                                                                                                                                                                                                                                      Wathen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPITVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QPTIVKTKNYTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRIPNKKPGKKTITIKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTEEPTINTTKTTTT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTEBPTINTKTNITTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The respiratory syncytial virus (RSV) G protein can be used in vaccines by inserting the G protein gene into a non-replicating vector. The G protein is placed under the control of alternating vector. The G protein sequences, for example the chimeric G protein signal and expression sequences, for example the chimeric G protein c produced may also comprise the signal peptide of tissue plasminogen activator (tPA). The recombinant vector may also comprise sequences upstream of the G protein gene which enhance the G proteins immunoprotective ability. The resulting immunogenic composition will generate antibodies directed against the RSV G protein when administered to a host organism. The composition is useful as a vaccine to immunise against RSV-associated disease, particularly resulting in a balanced Th/772 immune response and for raising Ab, by usual immunisation and cell fusion methods. This truncated G protein is secreted since it lacks a transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HKVTLTTAIIQDATSQIKMTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic composition for generating antibodies against respiratory syncytial virus - comprises non-replicating vector containing the protein G sequence, useful in protective vaccines and to raise antibodies for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20; Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.6%; Score 1229; DB 20; Leasure 10.0%; Pred. No. 1e-88; Indels
vaccine; immune response; immunogenicity; tPA; antibody; tissue plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP90441 standard; protein; 681 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Fig 3; 67pp; English.
                                                                                                                                                                                                                                                                                           Li X, Sambhara S;
                                                                                                                                                                              98WO-CA00697.
                                                                                                                                                                                                                97US-0896442.
                                                          Respiratory syncytial virus
                                                                                                                                                                                                                                                     (CONN-) CONNAUGHT LAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
es 232; Conservative
                                                                                                                                                                                                                                                                                                                                WPI; 1999-132254/11.
N-PSDB; AAX08422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 AA;
                                                                                                                                                                          16-JUL-1998;
                                                                                                                                                                                                                18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1989
                                                                                             W09904010-A1
                                                                                                                                                                                                                                                                                         Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Klebsiella
                                                                                                            Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB67771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB6777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FIISANHKVILITVIVQTIKNHTEKNITTVILQVPPERVSSSKQPTTTSPIHTNSATTSP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LCKSICKTIPSNKPKKKPTIKPTNKPTTNKRDPKTPAKTTKKETTTNPTKKPTLTT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GVKSNLQPITVKTKNTITTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCWAICKRIPNKKPGKKTTTKPTKKPTFKTT-KKDLKPQTTKPKEVPTTKPTEBPTINTT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ၀
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSKHKNQRTARTLEKTWDTLNHLIVISSCLYRLNLKSIAQIALSVLAMIISTSLIIAAII 60
                                                                                                                                                                                                                                                      Treatment of respiratory synctial virus infection (RSV) using Annexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 KTNITTLLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::|: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                            The specification describes a product which antagonizes binding of respiratory synctial virus (RSV) G-protein to annexin II or L-selectin, or causes a decrease in cell surface levels of annexin II or L-selectin. Such products are used in the manufacture of a medicament for use in prevention or treatment of RSV infection. The present sequence represents a RSV G-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carrier; G protein; RSV; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSV G protein peptide G2Na and diphtheria anatoxin peptide DTb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
49.9%; Score 771; DB 22; Length 299;
Best Local Similarity 54.7%; Pred. No. 1.3e-52;
Matches 162; Conservative 36; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diphtheria anatoxin; immune response; antigen; hypersensitivity response; vaccine; infection;
                                                                                                                                                                                                                                                                                                                  Disclosure; Page 71-73; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP97862 standard; protein; 361
                                                                                                                                                                                                                                                                               II or L-selectin derivatives
                                         23-OCT-2000; 2000WO-GB04084.
                                                                                   99GB-0024990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-2001; 2001FR-0009733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry
                                                                                                                           (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          syncytial
                                                                                                                                                                   Bird M;
                                                                                                                                                                                                             WPI; 2001-316238/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 AA;
                                                                                   21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FR2827606-A1
                                                                                                                                                                   Malhotra R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Respiratory
26-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP97862
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PNKKPGKKTTTKPTKKPTFKTTTKOHKPQTTKPKEVPTTKP---GSINLDMDVIRDKTKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a fusion protein comprising a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide generates an immune response against any antigen coupled to it, and and has a negative, immediate hypersensitivity response. Diphtheria anatoxin derived peptides, when modified to lack at least one cysteine residue, are useful as carrier peptides. Deletion of Cys residues in anatoxin peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal infections, or cancers and to generate, or increase, an immune response against infectious agents or tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition; RSV; RSV infection; lung; respiratory tract; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVKTKNITTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 PNKKPGKKTTTKPIKKPTFKTTKKDLKPOTTKPKEVPTTKPTEEPTIN------TTKT
                                                                                                                                                                                                                                                                                                               New peptide derived from diphtheria anatoxin, useful as carrier in vaccines, lacks at least one Cys residue, also related nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KIESLKEHGPIKNKMSESPNKTVSEEKAKQYLEEFHQTALE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 NITT-----TLINNITGNPKLTSQMETFHSTSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.6%; Score 580; DB 24;
70.8%; Pred. No. 1.6e-37;
tive 5; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 27-28; 42pp; French
                                                                              (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kīebsiella pneumoniae.
Respiratory syncytial virus.
20-JUL-2001; 2001FR-0009733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99FR-0011888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 114; Conservative
                                                                                                                                                            Nguyen NT,
                                                                                                                                                                                                                                 WPI; 2003-241969/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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120 ----
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP97863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                XXX88888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                             The present sequence represents a fusion protein comprising a Klebsiella pneumoniae outer membrane protein A (OmpA) designated P40 and a respiratory syncytial virus (RSV) antigon. Enterobaccerium OmpA proteins, associated with an immunogenic peptide from RSV are used to prepare a nasal composition that induces a protective response, against RSV infection in the upper and lower (lung) respiratory tract. OmpA potentiates the immune response to some immunogenic peptides, eliminating the need for adjuvants. The method is useful for producing vaccines for prevention or treatment of RSV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RONKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPCKKTTTKPTKKPTFKT 210
                                                                                                                          Vaccine against respiratory syncytial virus, comprises enterobacterial outer membrane protein and viral immunogen, provides protective response throughout the respiratory tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAPDRRVEIEVKGYKEVVTQ-----PQGPG-----DPMTVKTKNTTTTQTQPSKPTTKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTQDPQLGISFSNLSELTSQTTTILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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vaccines, lacks at least one Cys residue, also related nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carrier; G protein; RSV; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
37.1%; Score 572.5; DB 22; Length 452;
Best Local Similarity 76.1%; Pred. No. 8.2e-37;
Matches 108; Conservative 5; Mismatches 18; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSV G protein peptide G2Na and diphtheria anatoxin peptide DTa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diphtheria anatoxin; immune response; antigen; hypersensitivity response; vaccine; infection;
                                                                                                                                                                                                                                Example 2; Page 31-32; 39pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKKDLKPQTTKPKEVPTTKPTE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP97861 standard; protein; 291 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-2001; 2001FR-0009733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-2001; 2001FR-0009733
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  Corvaiea N, Goestch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-241969/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 AA
                                                                        N-PSDB; AAF80153
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                                         The present sequence represents a fusion protein comprising a peptide derived from the G protein of Respiratory syncytial virus (RSV) linked to a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide generates an immune response against any antigen coupled to it, and and has a negative, immediate hypersensitivity response. Diphtheria anatoxin derived peptides, when modified to lack at least one cysteine residue, are useful as carrier peptides. Deletion of Cys residues in peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal infections, or cancers and to generate, or increase, an immune response against infectious agents or tumour cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diphtheria anatoxin; immune response; antigen; carrier; G protein; hypersensitivity response; vaccine; infection; RSV; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSV G protein peptide G2Na and diphtheria anatoxin peptide DTaDTb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----MENF---SYHGTKPGYVDSIQKGIQKPKS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 36.6%; Score 564.5; DB 24;
67.1%; Pred. No. 2e-36;
ive 10; Mismatches 21; ]
Disclosure; Page 26-27; 42pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP97863 standard; protein; 548 AA.
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Corynebacterium diphtheriae.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 67.1
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                     291 AA;
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349 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein;
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                                                                                                                                                                                           Sequence
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to a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin and and has a negative, immediate hypersensitivity response. Diphtheria anatoxin derived peptides, when modified to lack at least one cysteine residue, are useful as carrier peptides. Deletion of Cys residues in anatoxin peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal infections, or cancers and to generate, or increase, an immune response against infectious agents or tumour cells.
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                                                                                                                                                                                                                130 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRI
                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus; protein G; carrier protein; immunogenicity; increase; enhance; vaccine; anti-viral; human serum albumin; binding; immunostimulation; respiratory syncytial virus; fusion protein.
                                                                                                                                                                                         23;
                                                                                                                                                              Query Match 36.6%; Score 564.5; DB 24; Length 548; Best Local Similarity 67.1%; Pred. No. 4.4e-36; Matches 110; Conservative 10; Mismatches 21; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcal protein G fragment BB fused to RSV hapten G2A
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                                                                                                                                                                                                                                                                                                                  248 LINNTIGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSS 291
                                                                                                                                                                                                                                                                                                                                        Stahl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric Streptococcus sp.
Chimeric Respiratory Syncytial Virus
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/label= BB
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/label= G2A
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                                                                                                                                        548 AA;
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                                                                                                                                        Sequence
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                                                                                                                                                              Query Match
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PNKPNNDFHFEVPNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ammonium salt; immunogen; antigen; syncytial virus infection;
; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of fusion protein comprising 2 G protein fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 NGKTLKGETTTEAVDAATARSFNFPILENSM---TVKTKONTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                                                               103 NLSEITSQTTT--ILASTT-----PGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of quaternary aliphatic ammonium salt and immunogen or antigen to combat respiratory syncytial virus infections
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
albumin-binding protein - useful for preparing improved vaccines, e.g. against Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                     Length 349;
                                                                                                                                                                                                                                                                                                                                              Query Match 36.4%; Score 562; DB 17; Length 3 Best Local Similarity 78.1%; Pred. No. 4e-36; Matches 107; Conservative 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "G protein fragment of VRS"
                                                             Disclosure; Page 81-83; 102pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 KPQTTKPKEVPTTKPTE 232
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Respiratory syncytial virus
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The specification describes a method which uses quaternary aliphatic ammonium salts together with an immunogen or antigen to treat syncytial virus infections. The combination of the salt with the antigen or immunogen improves immunogenicity and equilibrates the Th1/Th2 immuno response. The method is used for the treatment of respiratory syncytial virus infections. The present sequence represents a fusion protein, comprising an albumin binding domain of the G protein of Streptococcus sp. fused to a G protein fragment of respiratory syncytial virus (VRS, long version). The fusion protein is used as an antigen in the method of the invention.
Claim 16; Page 22-23; 35pp; French.
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Sequence 349 AA;

103 NLSEITSQTTT--ILASTT----PGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP 155 156 PNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKXDL 215 273 PNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKPGKKTTTKPTKKPTFKTTKKDH 332 Query Match 349; Score 562; DB 22; Length 349; Best Local Similarity 78.1%; Pred. No. 4e-36; Matches 107; Conservative 10; Mismatches 10; Indels 10; Gaps 216 KPOTTKPKEVPTTKPTE 232 333 KPÓTTKPKEVPTTKPVD 349 Db qq ð à ð

Search completed: October 29, 2003, 17:38:00 Job time : 70.034 secs

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Drosophila melanogaster genome survey sequence TET3 end of BACR #8ACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit flu), genomic envisor contracts.
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Neoptera; Modotterygota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
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/note="vector: pCWVSPORT 6; lst strand cDNA was primed
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Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODAO11BE07QP1.
Location/Qualifiers
     Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; no bw sp, the same strain used for the BDGP pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 712)
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                                                                                                                                                                                                                                                                                                                                           Query Match
16.8%; Score 120; DB 29; Length 895;
Best Local Similarity 25.0%; Pred. No. 1.3e-09;
Matches 129; Conservative 186; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                           308 others
                                                                                                                                                                               /organism="Drosophila melanogaster"
|mol_type="genomic DNA"
|db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : TRT3"
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                                                                                                                                                                                                                                                                                                                                             363 AAGAATACCAAAAAAACCAGGAAAGAAAACCACCACCAAGCCTACAAAAAAACCAAC 422
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1180)
                                                                                                        303 GITIAACITIGIACCCIGCAGCAIAIGCAGCAACAAICCAACCIGCIGGGGCIAICIGCAA
                                                                                                                                                              243 TACAAAACGCCAAAACAAACCACCAAAACCAATAATGATTTTCACTTCGAAGT
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      Length 712;
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                                           Indels
Query Match
15.8%; Score 113; Lo 13, Best Local Similarity 14.1%; Pred. No. 1.7e-08;
Matches 57; Conservative 221; Mismatches 127;
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Totoki, Y., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Hatanabe, H. and Sakaki, Y.
Totoki, Y., Hatanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIEM), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(G-mail:chimpbesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library FTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                        GSS 04-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                           AG127412 946 bp DNA linear GSS 04-NOV-200
Pan troglodytes DNA, clone: PTB-138B06.R, genomic survey sequence.
AG127412
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB_Chimpanzee Male_BAC_Library"
a 35īc 31g 23 t 36 others
                                                                                                                                                                                                                                                                                                                              Fujiyama, A., Hattori, M., Toyoda, A., 'Totoki, Y., Watanabe, H. and Sakaki, Y. BaC end sequences of Library PTB Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-138E06.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Pan troglodytes
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          612 AAAAAGHYYNTKHHYTYY
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                                                                                                                                   DEFINITION
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AG127412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed
with a NotL-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized." 288 others
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                                                                                                                                                                                                              http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CSOCAP001BG06QPl&cluster=516.f. Contact
cgi-bin/cluster.cgi?eeq=CSOCAP001BG06QPl&cluster=516.f. Contact
Feng Liang Bmail : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenu Genoscope sequence ID : CSOCAP001BG06QPl.
Location/Qualifiers
                                                                              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 516.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 CACTACAAAACAACGCCAAAACAAACCACCAAAACCCAATAATGATTTTCACTTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.6%; Score 111.4; DB 13; Length 1180; 25.8%; Pred. No. 2.6e-08; cive 194; Mismatches 219; Indels 1;
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP001YM12"
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                                                                    Contact: Genoscope
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ORIGIN Query Match Best Local Similarity 24.8%; Pred. No. 5.4e-07; Matches 102; Conservative 164; Mismatches 144; Indels 1; Gaps 1; Qy 181 CAACCCACACAGTCAAGACTAAAAACACAAACAAACCCAAAACCCCAAAGCCCCACAACCCCAAACCCCAAACCCCAAACCCCAAACCCC	1::: :	CCTGCAGCATATGCAGCAACCAACCTGCTGGGGTATCTGC :: : - - - - - - - - - - - - -			RESULT 6 CNSO4ENY C CNSO4ENY C CNSO4ENY S19 bp DNA linear GSS 01-SEP-2000 DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone DEFINITION Tetraodon nigroviridis genome survey sequence. ACCESSION AL287287 VERSION AL287287 KERWORDS GSS; genome survey sequence. ACCESSION AL287287 AL287287 CASTWORDS GSS; genome survey sequence.	_	AUTHORS Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence JOERNAL Nat. Genet. 25 (2), 235-238 (2000) REDEINE 20296633 PUBMED 10835645 REFERENCE 2 AUTHORS Roset Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,	Fizames/C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. TITLE Characterization and repeat analysis of the compact genome of the JOURNAL Genome Res. 10 (7), 939-949 (2000) MEDLINE 20159837 PUBMED 10899143 REFERENCE 3 (bases 1 to 919) AUTHORS Genoscope. TITLE Direct Submission	JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Qy 315 ACCCTGCAGGATATGGAGGAACAATCGAACCTGCTGGGGCTATCTGCAAAGAATACCAA 374 Db 453 AAAACAAACATCGTCTCCCACAAACAACAAAAAAAAAAA	OY 435 CAAAAAGATCTCAAACCTCAAACCACTAAACCAAGGAAGTACCCACCAAGGCCAC 494	Db 633 AAACACACACAAAAAACCCACACACACAAACACACAC	Oy 615 AGGCAATCTAAGCCCTTCTCAAGTCTCCGAACATCCGAGCACCCATCACAACCCTCATC 674 Db 753 CAGCACCCCAAAAAAAACCCCCCCCCCCCAACAAAAAACAAC	SULT 5 S0073W/c CUS CUS CNS0073W CUS FINITION Drosophila melanogaster genome survey seque BACH4009 of RPCI-98 library from Drosophil fly, genomic survey sequence.			The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoxI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library	valuate bac clones, the entire in ation from the BACPAC Resource Ce ac.med.buffalo.edu/drosophila_bac alifiers brosophila melanogaster" genomic DNA" axon:7227" *R14D09"	/note="end : TET3" BASE COUNT 223 a 95 c 109 g 221 t 274 others

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     Contact: Genoscope
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BP 191 91006 EVRY cedex - This sequence by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8261. For more information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODG004CC08NP1&cluster=8262.f. Contact : Feng Liang Email : filiang@lifetech.com URL: http://fullength.invitrogen.com/ LIVYtroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODG004CC08NP1.
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- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                     /organism="Tetraodon nigroviridis"
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EWYR cedex - FRANCE (B-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-enf sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCGR digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACRAC Resource Center can be location/Qualifiers

location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR3Z19 of RPCI-98 library from Drosophila melanogaster (fruit AL071370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 AACAACACCAGGAGTCAAGTCAAACCTGCAACCCCACAACAGTCAAGACTAAAAACACAAC 212
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                                                  541 CTGCTCACCAACACACCACAGGAAATCCAAAACTCACAGGTCAAATGGAAACCTTCCAC
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ehydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db xref="taxon:7227"
/clone="BARCIG"
/clone="lb="RRCI-98"
/note="end : TET3"
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                                                                     AL531977
AL531977 Homo sapiens FETAL LIVER Homo sapiens CDNA clone CSODW003YD03 5-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSFORT_6; 1st strand cDNA
/note="Organ: liver; Vector: pCMVSFORT_6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and RcoRV sites of the pCMVSFORT 6
vector. Library was not normalized."

a 208 c 323 g 416 t 93 others
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                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8045.f For
http://www.genoscope.cns.fr/
http://www.genoscope.cns.fr/
fogi-bin/cluster.cd/leage-CS0DM003CB02QPI&cluster=8045.f. Contact :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DM003CB02QPI.
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14.0%; Score 99.8; DB 9; Length 1201;
Best Local Similarity 41.7%; Pred. No. 1.7e-06;
Matches 223; Conservative 52; Mismatches 260; Indels 0.
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/tissue_type="FRTAL_LIVER"
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Li, W.B., Gruber, C., J
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BX385076 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED HOMO Sapiens CNDA clone CSODL006YEL2 3-PRIME, mRNA sequence.
                                                                                               149 CTTCAACAACACCAGGGGTCAAGTCAAACCTGCAACCACAACAGTCAAGACTAAAAACA 208
                           89 AGCTIGGAAICAGCTICTCCCAAICTGTCTGAAATTACAICACAAACCACCACCATACTAG 148
                                                                                                                                                                                                                                                 269 CAAACAAACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCATAT 328
                                                                                                                                                                                                                                                                                    389 AGAAAACCACCACCAAGCCTACAAAAAACCAACCTTCAAGACAACCAAAAAAAGATCTCA 448
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http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CSODL006BC06NP1&cluster=4073.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODL006BC06NP1.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1100)

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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.ons.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4073.r For
                                            633 MAMINAMMININHHINGNTRIRINNINNINMHINNGNTRIRINNTMINAMMINNINMAAMMAMININ
                                                                                                                                                                         569 CAAAACTCACAAGTCAAATGGAAACCTTCCACTCAACCTCCGGAAGGCAATCTAAGCC
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                                                                                             into
                     453 TCAAACCACTAAACCAAAGGAAGTACCCACCACCAAGGCCCACAGAAGAGCCAACCATCAA 512
CAPACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCATATGCAG 332
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 753)
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BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3806.r For
http://www.genoscope.cns.fr/
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cSobH001DC02NP1scluster=3806.r. Contact :
Feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBH001DC02NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

29 c 99 g 264 t 308 others
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                                                                                                                                                                                                                                                                                               513 CACCACCAAAACAAACATCACAACTACACTGCTCACCAACAACACC 558
                                                                                                                                                                                                                                                                                                                     /clone="CSODH001YF04"
/tissue_type="T CELLS (JURKAT CELL LINE)"
/cell_line="JURKAT CELL LINE"
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/db_xref="taxon:9606"
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/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
175 c 126 g 196 t 170 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -
                                                                                                                                                                                                                                                                                                                                       266 CACCAAACAAACCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCA 325
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae; Drosophila.
1 (bases 1 to 1097)
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                                                                                                                                                                                                          13.5%; Score 96.2; DB 13; Length 38.9%; Pred. No. 6.5e-06; ive 72; Mismatches 190; Indels
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                  clone="CSODL006YE12"
db_xref="taxon:9606"
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CNS012Z4/c
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http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBFH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGCTATCTGCAAAAGAATACCA 372
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                                                                                                                                                                           melanogaster"
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                                                                                                                                                                                                                                                                                                                       398
                                                                                                                                                                                   /mol_type="genomic DNA"
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/clone lib="brosBAC"
/plasmid="pBeloBAC11"
                                                                                                                                                1. .1097
/organism="Drosophila
                                                                                                                             Location/Qualifiers
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119 c
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us-09-462-816-3.rst

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Web: www.genoscope.ons.fr.

Web: www.genoscope.ons.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial Gross Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial sogenic strain of Drosophila DNA provided by the BDGP from the isogenic strain of Drosophila DNA provided by used for the BDGP's pl and BST libraries. A more detailed description of the library filters for hybridization from the BACPAC Resource Center can be location/Qualifiers

Location/Qualifiers
                                                                                                                          CNSOOLOO 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR32D23 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 TCTCCAATCTGTCTGAAATTACATCACAACCACCATACTAGCTTCAACAACACCAG
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Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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18.5%; Pred. No. 1e-05;
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/db_xref="taxon:7227"
                                                                                                                                                                               genomic survey sequence.
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/note="end : TET3"
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                       445 AACACACAAATAAAA 459
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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47.1%; Pred. No. 1.1e-05;
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                                                     Drosophila melanogaster (fruit fly)
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/clone lib="RPCI-98"
/note="end : T7"
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AL053801
AL053801.1 GI:4935176
GSS.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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BM 191 91006 EVRY cedex - France
EM 191 91006 EVRY cedex - France
Invitrogen. This sequence balongs to sequence cluster 5355.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0CAP003DF06NP1&cluster=5355.r. Contact:
Feng Liang Bmail: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0CAP003DF06NP1.
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/clone_lib="Homo sapiens THYMUS"
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1 (bases 1 to 899)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                    CAAACATCACAACTACACTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTC
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llarity 43.6%; Pred. No. 1.2e-05;
Conservative 62; Mismatches 227; Indels 3
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|db xref="taxon:9606"
|clone="CS0CAP003YL12"
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KEYWORDS
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completed: October 30, 2003, 01:15:25 le : 1946.71 secs

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SEQUENCE CHARACTERISTICS:
LENGTH: 15223 base pairs
TYPE: nucleic acid
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Sequence 10, Appl
Sequence 2, Appli
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                                                                                                     October 30, 2003, 00:01:13 ; Search time 240.957 Seconds (without alignments) 8070.528 Million cell updates/sec
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1 cacaaagtcacactaacaac.....gtagttattaaaaaaaaa
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-844-645-4

US-09-827-688-10

2 US-10-312-841-2

US-09-878-574-4304

US-10-311-455-1056

US-10-311-455-1056

US-10-311-455-1670

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US-09-878-574-4306

US-09-878-574-4306

US-09-878-574-4306

US-09-111-455-675

US-10-311-455-675
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                                                                                                                                                                                                                                                                                                           1811591 seqs, 1359896290 residues
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Maximum Match 100%
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                                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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		e					9		•			_		_					Secr	Segr	Sear	Sear	2 Secr	Sec	_		36 Sear	400 Sequ	
US-09-878-574-431	US-10-311-455-1669	US-10-029-386-20723	US-10-311-455-2004	US-10-311-455-17	US-10-240-453-187	US-10-239-676-165	US-10-029-386-20	US-10-017-161-18	US-10-311-455-1931	US-09-864-761-19241	US-09-864-761-251	US-09-864-761-20241	US-09-864-761-347	US-10-311-455-179	US-10-240-485-45	US-10-311-455-401	US-10-311-455-26	US-10-311-455-378	US-10-240-453-20	US-10-239-676-12	US-10-240-453-54	US-10-239-676-52	US-10-240-453-32	US-10-311-455-78	US-09-864-761-26582	US-10-311-455-47	US-10-311-455-11	US-10-311-455-24	
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74	73.4	72.8	72.8	72.2	72.2	72.2	71.8	71.8	71.8	71.4	71.4	71.2	71.2	71	70.8	70.6	70.6	70.4	70.4	70.4	70.4	70.4	70.2	70.2	70	70	9.69	9.69	
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ALIGNMENTS

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Sequence 1, Application US/09847173
Publication No. US20020182228A1
GENERAL INFORMATION:
APPLICANT: Collins, Peter L.
TITLE OF INVENTION: PRODUCTION OF INFECTIOUS RESPIRATORY
SYNCYTIAL VIRUS FROM CLONED NUCLEOTIDE SEQUENCES
                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Townsend and Townsend and Crew LLP
STREET: San Francisco
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYEE: FORPY: GAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IND PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/847,173
FILING DATE: 03-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NAMER: 08/720,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/POCKET NUMBER: 15280-250-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 95.3
Matches 470; Conservative
                                   COUNTRY: U.S.A.
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                                               ZIP: 10036
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                                                                               Score 654.8; DB 10; Length 15223;
Pred. No. 4e-164;
0; Mismatches 37; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Briles, David E.
McDaniel, Larry S.
Curiel, David T.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
ADMINISTERING PNEUMOCOCCAL, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS.
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
;
TOPOLOGY: linear

MOLECULE TYPE: other

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-847-173-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09844645
Patent No. US20020102242A1
GENERAL INFORMATION:
                                                                              Query Match
Best Local Similarity 94.8%;
Matches 677; Conservative
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259 ACCCCAACATACCTCACCCAGAATCCTCAGCTTGGAATCAGTCCCTCTAATCCGTCTGAA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 445.8; DB 10;
Pred. No. 5.8e-109;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                           NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REPERENCE/POCKET NUMBER: 454312-2450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,645
FILING DATE: 27-Apr-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/759,505
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) 5EQUENCE DESCRIPTION: SEQ ID NO: US-09-844-645-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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419

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Sequence 2. Application US/10312841
Publication Wo. US20030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des INTERENTE REPRENTE: 801/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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5548 TCTACATCAAATTCCACCAAAATACCCAATCACATGCTTAGTTATTCAAAAACTACA 5605
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                                                                                                                                                                                                                                                                                                                                               Length 3673778;
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                                                                                                                                                                                                                                                          OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                           12.0%; Score 85.8; DB 12; 47.0%; Pred. No. 3.1e-11; iive 0; Mismatches 372;
                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                        Query Match 12.0
Best Local Similarity 47.0
Matches 334; Conservative
                                                                                                                                                                                                                                                                                                  ; LOCATION: (379615)
US-10-312-841-2
                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
                                                                                                                                                                                                       LENGTH: 3673778
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                                                     APPLICANT: ORSON, FRANK
APPLICANT: CRSON, FRANK
APPLICANT: KINSEY, BERMA
APPLICANT: BERGAL, BALBER
APPLICANT: BERGAL, BALBER
TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION ITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
CURRENT APPLICATION NUMBER: US/09/827,688
CURRENT FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SEQ ID NO 10.
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                                                                                                                                                                                                                                                                                                                                      251; Indels
                                                                                                                                                                                                                                                                                                             DB 12;
                                                                                                                                                                                                                                                                                                          Score 300.4; DB 1
Pred. No. 1.5e-69;
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
       US-09-827-688-10

Sequence 10, Application US/09827688
Publication No. US20030165476A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 64.6%;
Matches 464; Conservative
                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: RSV
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160 CACCAAACCACGCAAACAACAAAC 131
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ORGANISM: Artificial Sequence
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Best Local Similarity 48.7%;
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                                                                                 Sequence 4304, Application US/09878574

Sequence 4304, Application US/09878574

Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT PELICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1990-06-14

PRIOR APPLICATION NUMBER: 09/333,535

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 4304

LENGTH: 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTACATCACAAAC-CACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 IGCAACCCACAACAGICAAGACTAAAAACACAAACAAACCCAAACACAAACAGCAAGC 238
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                        2;
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Query Match
11.7%; Score 83.6; DB 10; Length 'Best Local Similarity 48.4%; Pred. No. 2.7e-12;
Matches 276; Conservative 0; Mismatches 292; Indels
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure

: LOCATION: (1)...(793)

: OTHER INFORMATION: unsure at all n locations

: OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-C11

US-09-878-574-4304
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                                                                RESULT 5
US-09-878-574-4304/c
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## Sequence 1076, Application US/10311455

### Sequence 1076, Application US/10311455

### Publication No. US20030143606A1

### GENERAL INFORMATION:

### APPLICANT: OLEK, Alexander

### APPLICANT: DEFENBROCK, Christian

### APPLICANT: DEFENBROCK, Christian

### APPLICANT: DEFENBROCK, Christian

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109 AATCTGTCTGAAATTACATCACAAACCACCATACTAGCTTCAACAACACCAGGAGTC 168
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FRATURE:
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; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: PIEPENBROCK, Christian
; TILLE GP. INVERTION: Diagnosis of Diseases Associated with
; TILLE OF INVERTION: Metastasis
; FILER REPRENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; FRIOR PILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 2000-06-07
; PRIOR FILING DATE: 2000-06-07
; PRIOR FILING DATE: 2000-09-01
; ROOR APPLICATION NUMBER: DE 10043826.1
; RUGHER PRICH DATE: 2000-09-01
; RUGHER PRICH DATE: 2000-09-01
; RUGHER OF TILING DATE: 2000-09-01
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Pred. No. 4e-11;
0; Mismatches 269;
                                                                                                              5386 AAAAAAAAATAAAATCTCCTCC
                                                                       589 GAAACCTTCCACTCAACCTCCTCC
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Publication No. US20030148327A1
GENERAL INFORMATION:
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Best Local Similarity 46.64
Matches 235; Conservative
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LOCATION: (5837..)
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                                                                                             US-10-311-455-1056/C

Sequence 1056, Application US/10311455
Publication No. US20030143606A1
Sequence 1056, Application US/10311455
Publication No. US20030143606A1
SENDERAL INFORMATION:
APPLICANT: PIERBENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DC12-16
PRIOR FILING DATE: 2002-12-16
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-01
NUMBER: DE 10043826.1
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1056
LENGTH: 16167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 AATCTGTCTGAAATTACATCACAAACCACCATACTAGCTTCAACAACAACAGGAGTC 168
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5570, 5573, 5577..5578, 5592, 5732
c or t
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11.4%; Score 81.4; DB 12; Length 16167;
Best Local Similarity 46.6%; Pred. No. 4e-11;
Matches 235; Conservative 0; Mismatches 269; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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COTHER INFORMATION: n is a or g or c or US-10-311-455-1056
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is a or g or
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: 4003, 5529,
OTHER INFORMATION: n
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NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.0%; Score 78.8; DB 12; Length 1972; Best Local Similarity 46.5%; Pred. No. 7.8e-11; Matches 264; Conservative 0; Mismatches 302; Indels 2;
                                                                                                                                                                                    Sequence 1981, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUWA, MAZIKO

APPLICANT: AKIYAMA, YUTAKA

APPLICANT: ARIYAMA, YUTAKA

APPLICANT: ARUYAMA, YUTAKA

APPLICANT: ARUYAMA, YUTAKA

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0152

CURRENT FILING DATE: 2002-12-18

FRIOR APPLICATION NUMBER: JP 2001/246789

PRIOR PILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 1981

LENGTH: 1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified base

LOCATION: (1319)..(1328)

GTHER INFORMATION: a, t, c, g, unknown or other

19:10-017-161-1981
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                                                                                                           2931 AAAAACAAAAAAAAAACAAA 2912
                                                                         573 ACTCACAAGTCAAATGGAAA 592
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LOCATION: (975)..(994)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (201)..(1772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1)..(1972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: source
LOCATION: (1)..(
                                                                                                                                                                                  US-10-017-161-1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: CDS
LOCATION: (201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                 Sequence 1670, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5506 AACCTITIACCCAAACCCCATTACATCATCACCTAACCTAAACCTCTACCAAACCTAA 5447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 AACAACACCAGGAGTCAAGTCAAACCTGCAACCCACAACAGACTAAAAACACAAGAC 212
529 ATCACAACTACACTGCTCACCAACAACACCCACAGGAAATCCAAAAACTCACAAGTCAAATG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 AACCACCACCAAGCTACAAAAAAACCAACCTTCAAGACAACCAAAAAAGGATCTCAAAACC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 TCAAACCACTAAACCAAAGGAAGTACCCACCACCAAGCCCACAGAAGAAGCCAACCATCAA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 CAAACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCATATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80; DB 12; Length 6668;
Pred. No. 6.4e-11;
0; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
SRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
SRION FILING DATE: 2000-09-01
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COCATION: 1936
US-10-311-455-1670
                                                                                                                                                                              5386 AAAAAAAAATAAATCTCCTCC 5363
                                                                                                                                            589 GAAACCTTCCACTCAACCTCCTCC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 48.9%;
Matches 215; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                    .10-311-455-1670/c
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Sequence 2109. Application US/09983965

Patent No. US20020137160A1

GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILE OF INVENTION: WUMBER: US/09/983,965
CURRENT APPLICATION NUMBER: US 09/465,231
FRIOR PELLING DATE: 1999-12-15
FRIOR FILING DATE: 1999-12-15
FRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5912
FROM PROPERTY OF SEQ ID NOS: 5912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 CAACCITCAAGACAACCAAAAAAGATCICAAACCICAAACCACTAAACCAAAGGAAGIAC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AAATTACATCACAACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 IGCAACCCACAACAGTCAAGACTAAAAACACAACAACAACCCAAAACACCCAGCAAGC
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                                                     545 TCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 76.4; DB 10; Length
Pred. No. 1.9e-10;
0; Mismatches 237; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DIA

ORGANISM: Bos taurus
FRATURE:

INAME/FEX: unsure

LOCATION: (335)

OTHER INFORMATION:

OTHER INFORMATION:

COPER INFORMATION:

OTHER 105-01-K1-A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   539 CACTGCTCACCAACAACACACAGGAAATCCAAAA 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 47.9%;
Matches 218; Conservative (
                                                                                                                      RESULT 12
US-09-983-965-2109/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Mucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/09/878,574
FILE REFERENCE: 2001-12-21
PRIOR PAPLICATION NUMBER: 09/333,535
PRIOR PAPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 4296
LENGTH: 576
484 ACCAAGCCCACAGAAGAGCCAACCATCAACACCAACAAAAAAACAACAACTACACTG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244
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                                                                                                                                                                                          604 ACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCATCA
                                                                                                                544 CTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 TTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGGCTATCTGCAAAA
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clarity 50.9%; Pred. No. 1.7e-10;
Conservative 0; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLATION: (1)...(576)
COTHER INFORMATION: unsure at all n locations
COTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-G1
US-09-878-574-4296
                                                                                                                                                                                                                                                                                                       1345 ccaccaccarcaccaccarcaccac
                                                                                                                                                                                                                                                                   CAACCCTCATCTCCACCCAACACAC 691
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4296, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 207; Conserva
                                                                                                                                                                                                                                                                                                                                                                                    US-09-878-574-4296/c
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Sequence 4312/Application US/09878574

Sequence 4312, Application US/09878574

Patent No. US2002011054831

GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION NUMBER: 09/333,535

NUMBER OF SEQ ID NOS: 15775

LENGTH: 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 AAACCACCACATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTGCAACCCACAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 CAGTCAAGACTAAAAACACCAAACAACCCAAAACACCCAGCAAGCCCACTACAAAAC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 AACGCCAAAACAAACCACCAAAACAAAACCCAATAATGATTTTCACTTCGAAGTGTTTAAC- 309
413 CACARCACARACORARCACARACORACORACORARACORCOROCARCACORCARACORARACORA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 TITIGIACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGCTATCTGCAAAAGAATA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 CACCCCANAACCAAAACAACAACAAAAAAACCAACACCCCAAACAAACAACCAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCCACCACCAA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 GCCCACAGAGAGCCAACCATCAACACCACCAAAAAAAAACATCACAAACTACACTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAAACAAAAAACCAGGAAAGAAACCAC-CACCAAGCCTACAAAAAAAACCAACCTTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.5%; Score 75; DB 10; Length 577; Best Local Similarity 50.0%; Pred. No. 4.6e-10; Matches 232; Conservative 0; Mismatches 230; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(577)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-G11
                                                                    140 CNANNANNANNCNNNGANNACCNANAGANNAC 110
                                661 TCACAACCCTCATCTCCACCCAACACACAC 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-10-311-455-675/c
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               Sequence 4306, Application US/09878574

Sequence 4306, Application US/09878574

Sequence 4306, Application US/09878574

Sequence 4306, Application US/09878574

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR FILING DATE: 1990-06-14

NUMBER OF SEQ ID NOS: 15775

LENGTH: 1030
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                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)...(1030)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-D11
                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Glycine max
             JS-09-878-574-4306/c
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
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US-09-878-574-4306
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Publication No. US2003014366A1

GENERAL INFORMATION:
APPLICANT: OLEK, ABexander
APPLICANT: OLEK, ABexander
APPLICANT: OLEK, ABexander
APPLICANT: PIERENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: UNDER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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Sequence 675, Application US/10311455
Publication No. US20030143606A1
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ORGANISM: Artificial Sequence
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Search completed: October 30, 2003, 03:23:54 Job time : 246.957 secs

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TOPOLOGY:
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*

/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/RECTWS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTWS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTWS_COMB.seq:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-818189D-7

US-08-814-639E-7

US-08-447-963H-7

US-08-467-963H-7

US-08-467-963H-7

US-08-818-189D-28

US-08-818-189D-28

US-08-82-34HD-28

US-08-82-34HD-28

US-08-82-34HD-28

US-08-82-403H-1

US-08-82-403H-1

US-08-82-403H-1

US-08-82-403H-1

US-08-836-501-1

US-08-836-501-1

US-08-836-501-1

US-08-836-501-1

US-08-64-289-1

US-09-654-289-1

US-09-654-289-1

US-09-654-289-1

US-09-654-289-1

US-09-654-830-1

US-09-654-830-1

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Maximum Match 100%
Listing first 45 summaries
                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                  Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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GENERAL INPORMATION:

APPLICANT: KLEIN, Michel H
APPLICANT: KLEIN, Michel H
APPLICANT: DI, KUN-Pan
APPLICANT: DI, KUN-Pan
APPLICANT: BRASYSHYM, MANY E
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMBRIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38 A
ADDRESSES: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
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COUNTRY: Canada
ZIP: M5G 1R/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
                                                 US-09-654-289-3
US-09-654-289-3
US-09-654-289-3
US-08-721-979A-14
US-08-721-979A-14
US-09-624-289-14
US-09-68-836-14
US-09-68-836-14
US-08-836-501-23
US-09-654-289-23
US-09-654-289-23
US-09-654-28-23
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REPERENCE/DOCKET NUMBER: 1038-474 MIS:jb
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-836-501-2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,189
FILING DATE: 06-07N-1993
PRIOR APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-07N-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-07N-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08467963C
Patent No. 5968776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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206 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGACGAAGATCAAGAAGATGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,189D
FILING DATE: 16-APR-1997
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
RICHARD AATE: 06-JAN-1993
ATPONENTY/AGENT INFORMATION:
ANAMER OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF 
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100.0%; Pred. No. 1.9e-185;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                    NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE DOCKET NUMBER: 1038-687 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPRAN: (416) 595-1155
TELEPRAY: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 715; Conservative
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Patent No. 5998169
GENERAL INFORMATION:
APPLICANT: EVENN Michel H
APPLICANT: EVENN MICHEL H
APPLICANT: EVENN MICHEL H
APPLICANT: EVENN MICHEL H
TITLE OF INVENTION: MICHERIC PROTEIN WHICH CONPERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBULNEY
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                                                                                                                       1 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGAAGAACACA
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                                Length 920;
                        Query Match
100.0%; Score 715; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.9e-185;
Matches 715; Conservative 0; Mismatches 0;
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STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Toronto STATE: Ontario
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US-08-838-189D-7
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,639E
FILING DATE: 14-NOV-1994
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APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
FLIASSIFICATION: 924
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy
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M5G 1R7
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STATE: Ontario
COUNTRY: Canada
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                                         806 TCAACCTCCTCCTCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCTCGAGCACCACA 865
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                                                                                                     GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: DV. Run-Pan
APPLICANT: BMASYSHYN, MARY E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,344D
FILING DATE: 07-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,639
FILING DATE: 06-JAN-1992
ATFORNEY/AGANT INFORMATION:
NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,973
REFERENCE/POCKET UNBER: 24,973
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                          ; Sequence 7, Application US/08852344D; Patent No. 6017539
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 715; Conservative
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STREET: be...
Tary: Toronto
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COUNTRY: Canada
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326 ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG 385
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APPLICANT: Klein, Michel H
APPLICANT: Every Michel H
APPLICANT: Busyshyn, Mary B
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
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330 University Avenue, 6th Floor
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US-08-467-969A-7
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Best Local Similarity 100.0%; Pred. No. 1.9e-185;
Matches 715; Conservative 0; Mismatches 0; Indels
                                    RADES SEGNATE, Michael I
REGISTRATION NUMBER: 24,973
REPERENCE DOCKET NUMBER: 1038-391 MIS
TELECOMMUNICATION INFORMATION:
TELEPAN: (416) 595-1153
TELEPAN: (416) 595-1163
TELEPAN: 065-4867 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: mucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-639E-7
FILING DATE: 06-JAN-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: Patentin Release #1.0, Version #1.25
SUGTAME: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,969A
FILING DATE: 06-JUN-1995
CLASSIPICATION: 435
PRIOR APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JN-1993
CLASSIPICATION NUMBER: US 08/2017.1
FILING DATE: 06-JAN-1992
CLASSIPICATION NUMBER: 24-973
RPPLICATION NUMBER: 24-973
APPLICATION NUMBER: 24-973
FILING DATE: 06-JAN-1992
CLASSIFICATION: Micheel I
REGISTRATION NUMBER: 24-973
FILING DATE: (416) 595-1165
TELEPHONE: (416) 595-1165
TELEFRAX: (416) 595-1163
TELEFRAX: (416) 595-1163
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100.0%; Pred. No. 1.9e-185;
tive 0; Mismatches 0;
                                                                                      APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Dw, Run-Pan
APPLICANT: Bwasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
Sequence 7, Application US/08467969A
Patent No. 6168786
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Florm:
COMPUTER
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Best Local S:
Matches 715
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                                                                                                                                                                                                                626 accircaagacaaccaaaaagarcicaaaccicaaaccacraaaccaaaagaagracc 685
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                                                                                   566 AAAAGAATACCAAAAAAAACCAGGAAAGAAAACCACCACCAAGCCTACAAAAAAACA 625
                         506 GTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGCTATCTGC
                                                                                                                                                                       421 ACCTTCAAGACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,961A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
PRIOR APPLICATION ADATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: GB 9200117.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE DOCKET NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
TELEFRAX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6TH Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08467961A Patent No. 6171783
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STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                                                                                                                                           Length 920;
                                                                                                                                                      100.0%; Score 715; DB 3; Length 92
100.0%; Pred. No. 1.9e-185;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08001554A
Patent No. 6225091
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Ewasyshyn, Mary E
ITILE OF INVENTION: Chimeric Immunogens
NUMBER OF SUCHENCES: 21
NUMBER OF SECUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                      LENGTH: 920 base pairs
TYPE: nucleic acid
TYRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: DNA (genomic)
US-08-467-961A-7
                                                                                                                                                                                             Matches 715; Conservative
SEQUENCE CHARACTERISTICS:
                                                                                                                                                         Query Match
Best Local Similarity
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46 CIGCICACCAACAACACCCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC 805
                                                                                                                                                                                                                                                                                                                               APPLICANT: KLEIN, Michel H
APPLICANT: ENGASYSHYN, Mary E
FILLS OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 ACCCCAACATACCTCCACGGATCCTCAGCATCAGCATCAGCTTCTCTCAATCTGTGAA
                                             601 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCAACAACATCCGAGCACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGAGCCAGATCAAGAACACA
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                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,963C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-JAN-192
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-DAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       US-08-467-963C-28
; Sequence 28, Application US/08467963C
; Patent No. 5968776
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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COUNTRY: Canada
ZIP: M5G 1R7
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-467-963C-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 446 ACTACAAAACAAGCCAAAACAAACCACCAAAACAAACCAATAATGATTTTTCACTTCGAA 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 715; DB 3; Length 920; 100.0%; Pred. No. 1.9e-185; Ative 0; Mismatches 0; Indels (
                                                                                                          MEDIUM TYPE: Floppy disk
COMEDTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,554A
FILING DATE: 06-JAN-1993
STREET: 330 University Avenue, 6th Floor CITY: Toronto
                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFREENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                 FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 065-24567 SIMBAS INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 920 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 715; Conservative
                                         STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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RESULT 10
US-08-852-344D-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/08838189D
Patent No. 5998169
GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: BYASYSHYN, MARY B
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
121 ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG 180
                      ATTACATCACAAACCACCACCATCATACTAGCTTCAACAACAACAACAGGAGTCAAGTCAAACCTG 378
                                                                   CAACCCACACAGTCAAGACTAAAAACACAACAACAACCAAACAACACAAACACAAGCCC 240
                                                                                                    379 CAACCCACAACAGTCAAGACTAAAAACACAACAACAACCAAAACACAAACCCAGCAAGCCC 438
                                                                                                                                        GIGITIAACITIGIACCCIGCAGCALAIGCAGCAACAATCCAACCIGCTGGGCTAICIGC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: 16-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCACAACCCTCATCTCCACCCAACACACACGCCAG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               859 TCACAACCCTCATCTCCACCCAACACACACACGCCAG 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sin & Meburney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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CLASSIFICATION:
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US-08-838-189D-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 ATTACATCACAAACCCCCCCATACTAGCTTCAACAACCCAGGAGTCAAGTCAAACCTG 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTACAAAACAACGCCAAAACAAACCACCAAAAAACAATAATGATTTCACTTCGAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 ACTACAAAACAACGCCAAAACAAACCCACAAACAAACCCAATAATGATTTTCACTTCGAA 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            739 crecricaccaacaacaccacacacaaarccaaaacrcacaagrcaaarccaaccrrccac 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          799 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCCA 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGAGCCAGATCAAGAACACA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGCCAGATCAAGAACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.3%; Score 696; DB 2; Lv
100.0%; Pred. No. 2.8e-180;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           661 TCACAACCCTCATCTCCACCCAACACACACGCCAG 696
                                                                                                                                                      REFERENCE/DOCKET NUMBER: 1038-687 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION UNMERS: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                         NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Lou.
                                                                                                                                                                                                                                                                                                                                          LENGTH: 894 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                         .vroLOGY: linear
US-08-838-189D-28
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499 GIGITTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGCTATCTGC 558
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                                                                                                      619 ACCTICAAGACAACCAAAAAAGAICTCAAACCICAAACCACIAAACCAAAGGAAGTACCC
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                                                                                                                                                    421 ACCTICAAGACCAAAAAAGAICICAAACCICAAACCACTAAACCAAAGGAAGTACCC
                                                                                                                                                                                                                                                   CTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28. Application US/08344639E

Patent No. 6033668

GENERAL INFORMATION:

APPLICANT: Klein, Michel H

APPLICANT: Ewasyshyn, Mary E

ITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS

ITLES OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRI

ITLES OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentle Release #1.0, Version #1.25
SOFTWARE: Patentle Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,639E
FILING DATE: 14-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIPICATION NUMBER: GB 9200117.1
PRIOR APPLICATION NUMBER: GB 9200117.1
PRIOR APPLICATION NUMBER: GB 9200117.1
PRIOR APPLICATION: 424
ATTOMNEY/GRENT: REORGANTION:
ANAME: GASSIPICATION: 424
ATTOMNEY/GRENT: REORGANTION:
ANAME: GASSIPICATION: 424
ATTOMNEY/GRENT: REORGANTION:
ANAME: GASSIPICATION: 424
ATTOMNEY/GRENT: REORGANTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 TCACAACCCTCATCTCCACCCAACACACACGCCAG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               859 TCACAACCCTCATCTCCACCCAACACAACACGCCAG 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Sim & McBurney
330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1038-391 MIS
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REGISTRATION NUMBER: 24,973
REBERENCE/DOCKET NUMBER: 1039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1153
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 28:
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ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toronto
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STREET: 33
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Patent No. 6017539
GENERAL INFORMATION:
APPLICANT: MICHEL H
APPLICANT: DU, Run-Pan
APPLICANT: BASYSHTN, MARY B
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCTIAL VIRUS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ELING DATE: US/08/852,344D
FILING DATE: 07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLIASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MACHAEL
REFERENCE/DOCKET NUMBER: 1038-688 MIS:jb
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                        STREET: Sim & MCBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                           ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Sequence 23, Application US/08801898A

GENERAL INFORMATION:

APPLICANT: Silverman, Robert H.

APPLICANT: Silverman, Robert H.

APPLICANT: Li, Guiying

TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE

TITLE OF INVENTION: OLIGONUCLEOTIDES EFFECTIVE TO TREAT RSV INFECTIONS NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
                                                                                                                                                        CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGCCAGATCAAGAACACA
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                                                                                                Length 894;
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                                                                                          Query Match 97.3%; Score 696; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 2.8e-180;
Matches 696; Conservative 0; Mismatches 0;
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LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
JODOLOGY: linear
US-08-344-639E-28
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US-08-801-898A-23
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                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM COMPALIDIE
OPERATING SYSTEM: DOS
SOFTWARE: FEASESO Version 2.0
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/801,898A
FILLING DATE: 18-FEB-1997
CLASSIFICATION: 514
ATTORNEY, AGENT INFORMATION:
NAME: POISBEAR, Brian M.
REGISTRATION NUMBER: 28,462
REFREENCE/DOCKET NUMBER: 8656-009
TELECOMPUNICATION INFORMATION:
TELECOMPUNICATION INFORMATION:
TELECOMPUNICATION INFORMATION:
TELECOMPUNICATION SEG-9741
TELECOMPUNICATION SEG-9741
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TELECOMPUNICATION SEG-9741
TELECOMPUNICATION SEG-9741
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 15222 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA FEATURE:
                                                                                                                    U.S.A.
                                                                                                                    COUNTRY:
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Patent No. 5993824
GENERAL INFORMATION:
FAPILICANT: Collins, Peter L.
APPLICANT: Mitchead, Stephen S.
APPLICANT: Juhasz, Katalin
TITLE OF INVENTION: PRODUCTION OF ATTENUATED RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS VACCINES FROM CLONED NUCLEOTIDE SEQUENCES
  421 ACCTTCAAGACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
                                                                                                9917 ACCCTCAAGACAACCAAAAAGATCCCAAACCTCAAACCACTAAATCAAAGGAAGTACCC
                                                                                                                                                                                                                                                                                    9797 CTACTCACCTCCAACACCACAGGAATCCAGAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                         9737 ICAACTICCTCCGAAGGCAATCCAAGCCCTTCTCAAGTCTCTACAACATCCGAGTACCCA
                                                                                                                                                      601 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                        9677 TCACAACCTTCATCTCCACCCAACACACACGCCAGTAGTTACTTAAAAACATA 9624
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,403A
FILING DATE: 15-ULL-1997
CLASSIFICATION NUMBER: US 60/047,634
PILING DATE: 23-MAY-1997
PRIOR APPLICATION NUMBER: US 60/046,141
PILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 60/021,773
PRIOR APPLICATION NUMBER: US 60/021,773
PILING DATE: 15-UUL-1996
ATTONERY/AGENT INPOMMATION:
NAMR: NAMR: SEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 17634-000510
ELECOMMUTICATION:
TELEPHONE: 206-467-9600
TELEPRAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,990
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nucleic acid
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LENGTH: 15223 base pa:
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COMPUTER READABLE FORM:
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GIGITCAACTITIGIACCCIGCAGCATAIGCAGCAACAAICCAACCIGCIGGGCIAICIGC 9978
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                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08962690

| Sequence 12, Application US/08962690
| Patent No. 6214805
| GENERAL INFORMATION:
| APPLICANT: Torrence, Paul F. |
| APPLICANT: Cirino, Nick M. |
| APPLICANT: Cirino, Nick M. |
| APPLICANT: Mark M. |
| APPLICANT: Mark M. |
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| APPLICANT: Mark M. |
| APPLICANT: MARK M. |
| FILING DATE: 1997-11-03 |
| EARLIER APPLICATION NUMBER: 06/011,725 |
| BARLIER APPLICATION NUMBER: 60/011,725 |
| BARLIER APPLICATION NUMBER: 60/011,725 |
| BARLIER PLING DATE: 1996-02-15 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NOS: 40 |
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                                                                                                                                                                                                                                                                91.6%; Score 654.8; DB 3; Length 15222; 94.8%; Pred. No. 1.5e-168; tive 0; Mismatches 37; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: respiratory syncytial virus
US-08-962-690-12
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Best Local Similarity 94.8
Matches 677; Conservative
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Patent No. 6264957
GENERAL INFORMATION:
APPLICANT: Collins, Peter L.
TITLE OF INVENTION: PRODUCTION OF INFECTIOUS RESPIRATORY
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                        Gaps
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                                                               Length 15223;
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                                                           Score 654.8; DB 2;
Pred. No. 1.5e-168;
0; Mismatches 37;
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                                                          91.6%;
                                                        Query Match
Best Local Similarity 94.8
Matches 677; Conservative
STRANDEDNESS: single
             TOPOLOGY: linear MOLECULE TYPE: CDNA
                         ; MOLECULE TYI
US-08-892-403A-1
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US-08-720-132-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSKIT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,132
FILING DATE: 27-SEP-1996
CLASSIFICATION NUMBER: US 60/007,083
FILING DATE: 27-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATMELSE, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
REGISTRATION NUMBER: 31,990
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Pred. No. 1.5e-168;
0; Mismatches 37;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 94.8
Matches 677; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: other
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Wed Nov

6666

Search completed: October 30, 2003, 01:17:38 Job time : 57.5382 secs

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October 29, 2003, 16:50:52; Search time 244.018 Seconds (without alignments) 7909.644 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	715	100,0		14	AAQ45686	Respiratory syncit
3	715	100.0		20	AAX08421	Membrane bound G r
4	629	92.2		œ	AAN70784	Sequence encoding
2	629	92.2	935	19		HRSV glycoprotein
9	657.4	91.9			AAQ29623	HSRV glycoprotein
c 7	654.8	91,6			AAX59703	Polynucleotide sec
89	654.8	91.6	15222	18	AAT78440	Human respiratory

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18 AAT63430 21 AAA88743 22 AAA88743 24 AAA28145 24 AAA738298 19 AAV73529 21 AAA88744 22 AAA7322914 24 AAA722914 20 AAX322914 20 AAX322914 20 AAX322913 20 AAX322913 20 AAX35271 20 AAX35271 20 AAX35271 20 AAX35271 21 AAY18279 20 AAX35271 22 AAE84711 22 AAE84711 22 AAE84711 23 AAT31647 24 AAX35271 27 AAX35271 28 AAX35271 29 AAX35271 21 AAY18280 20 AAX35271 21 AAY18280 21 AAX35271 22 AAE84711 23 AAX35271 24 AAX35271 25 AAX35271 26 AAX35271 27 AAX35271 28 AAX35271 29 AAX35271 21 AAX35271 21 AAX35271 22 AAX35272 23 AAX35271 24 AAX35271 25 AAX35271 26 AAX35271 27 AAX35271 28 AAX35271 28 AAX35271 29 AAX35271 20 AAX35271 21 AAX35271 22 AAX35271 23 AAX35271 24 AAX35271 25 AAX35271 26 AAX35271 27 AAX35271 28 AAX3527 28 AAX3527 2
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ALIGNMENTS

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AAX08422 standard; cDNA; 715

RESULT 1 AAX08422

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G protein; respiratory syncytial virus; RSV; recombinant vector;
vaccine; immune response; immunogenicity; tPA; antibody;
tissue plasminogen activator; ss.
                                                    G protein gene fragment of respiratory syncytial virus.
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/*tag= a
/product= "Secreted G protein"
                                                                                                                          Location/Qualifiers
                                                                                                        Respiratory syncytial virus (RSV).
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                                 28-JUN-1999 (first entry)
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                                                                                                                                                                                                                            18-JUL-1997;
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                 AAX08422;
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Claim 11; Figure 7A-7D; 80pp; English.
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13-JAN-1994
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                                                       Immunogenic composition for generating antibodies against respiratory syncytial virus - comprises non-replicating vector containing the protein G sequence, useful in protective vaccines and to raise antibodies for diagnosis
                                                                                                                                                  vaccines by inserting the G protein gene into a non-replicating vector. The G protein is placed under the control of alternative signal and expression sequences, for example the chimeric G protein produced may also comprise the signal peptide of tissue plasminogen activator (tPA). The recombinant vector may also comprise sequences upstream of the G protein gene which enhance the G proteins immunoprotective ability. The resulting immunogenic composition will agenerate antibodies directed against the RSV G protein when administered to a host organism. The composition is useful as a vaccine to immunise against RSV-associated disease, particularly resulting in a balanced Thi/Thz immune response and for raising Ab, usual immunisation and cell fusion methods.
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                                                                                                                                                                                                                                                                                                                                     Length 715;
                                                                                                                                        The respiratory syncytial virus (RSV) G protein can be
                                                                                                                                                                                                                                                                                                          Sequence 715 BP; 305 A; 240 C; 70 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                   100.0%; Score 715; DB 20;
100.0%; Pred. No. 1.4e-162;
tive 0; Mismatches 0;
                                                                                                                 Claim 8; Figure 3; 67pp; English.
 Sambhara S;
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                       WPI; 1999-132254/11
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                                  P-PSDB; AAW96314
Klein MH,
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Matches 715
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                                                                                        consists of two gene sequences which are linked and encode antigenic regions, these two sequences being derived from two different pathogens (parainfluenza virus (PIV) and respiratory syncitial virus (RSV)). The gene sequences that are particularly used are those which encode PIV-3 F and HN proteins (AAQ45683, AAQ45684) and RSV F a (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                   ATTACATCACAAACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG
                                          CAACCCACAACAGTCAAGACTAAAAACACAACAACCAAGCAAACACAAGCAGCAAGCCC
                                                     ACTACAAAACAACGCCAAAACAACCCCCAAACAAACCAATAATGATTTTTCACTTCGAA
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                                                                                                                                                                                                TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
                                                                                                                                                                                                                        G protein; respiratory syncytial virus; RSV; recombinant vector;
vaccine; immune response; immunogenicity; tPA; antibody;
                                                                                                                                                                                                                                                                                                                    Membrane bound G protein gene of respiratory syncytial virus.
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/*tag= a
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                                                                                                                                                                                                                                                                                        The respiratory syncytial virus (RSV) G protein can be used in vaccines by inserting the G protein gene into a non-replicating vector. The G protein is placed under the control of alternative signal and expression sequences, for example the chimeric G protein produced may also comprise the signal peptide of tissue plasminogen activator (tPA). The recombinant vector may also comprise sequences upstream of the G protein gene which enhance the G proteins immunoprotective ability. The resulting immunogenic composition will administered to a host organism. The composition is useful as a vaccine to immunise against RSV-associated disease, particularly resulting in a balanced Th1/Th2 immune response and for raising Ab, by usual immunisation and cell fusion methods.
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                                                                                                                                             Immunogenic composition for generating antibodies against respiratory syncytial virus - comprises non-replicating vector containing the protein G sequence, useful in protective vaccines and to raise antibodies for diagnosis
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                                           Sambhara
(CONN-) CONNAUGHT LAB LID
                                                                                    WPI; 1999-132254/11.
                                       Klein MH, Li X,
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                       CAACCCACAACAGTCAAGACTAAAAACACAACAACAACCCAAAACAACCCAGCAAGCCC
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/product= glycoprotein_G
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86WO-US02756.
92US-0897171.
97US-0854783.
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23-DEC-1986;
11-JUN-1992;
12-MAY-1997;
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                          806 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCCACAACATCTGAGCACCCA
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                                                                                                                                                                                                                  Sequence encoding human respiratory syncytial virus (HRSV) A2 strain G protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                        A novel plasmid which comprises a DNA sequence encoding this protein, and the protein itself, are claimed, for use as HRSV sectimes. The vactime can be administered to pregnant women or to women of child bearing age to stimulate maternal antibodies. Infants can also be vaccinated at 2-3 months of age. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccines for human respiratory virus - comprising proteins or fragment encoded by a DNA sequence coding for human respiratory syncytial virus proteins.
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                                                                                                                                                                                                                                                                                    Human respiratory syncytial virus (HRSV).
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(first entry)
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P-PSDB; AAP70845.
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Best Local Similarity
Matches 680; Conserv
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05-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                        Production of human respiratory syncytial virus glyco-protein F or (
- by culturing eukaryotic host cells transfected with corresponding
DNA.
                                                                                                                                                                                                                                                                                   The present sequence was used in the development of a novel method for the production of human respiratory syncytial virus (HRSV) glycoprotein G (GpG). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV gpF or gpG. The gp can be used to prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
92.2%; Score 659; DB 19; Length 935;
Best Local Similarity 95.1%; Pred. No. 4.5e-149;
Matches 680; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 935 BP; 383 A; 293 C; 100 G; 159 T; 0 other;
                                                                                                                                                                                                                               Example 1; Columns 27-28; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccines against HRSV.
                              WPI; 1998-144802/13.
P-PSDB; AAW47605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences of mRNA encoding HRSV structural proteins are given in AAQ2952-2-6. The proteins are P, G, 22K, 9.5K and major capsid protein N. The sequences and encoded proteins are useful for preparing vaccines against HRSV. The vaccines can be used to confer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                            Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K; major capsid protein; N; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prime the reverse transcription reaction for making the first strand of the CDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunity against respiratory tract infections on human subjects. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= c
/note= "oligonucleotide used to specifically
/note= "oligonucleotide used to specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccines for human respiratory virus - include structural ge coding for native structural viral proteins and immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Indelв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "oligonucleotide used to probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 935 BP; 382 A; 294 C; 100 G; 159 T; 0 other;
                                                                                                                                                                                                                                                                                                       Human respiratory syncytial virus strain A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full length cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 18; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/label= G_protein
AAQ29623 standard; DNA; 935 BP.
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                                                                                                                              (first entry)
                                                                                                                                                                              HSRV glycoprotein G (gpG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 679; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc feature
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                                                                                                   25-MAR-2003
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                                                                                                                              03-MAR-1993
                                                     AAQ29623;
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Best Local S
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The specification describes a composition comprising a polynucleotide consisting of an antisense oligonucleotide containing a hydroxy group, complementary to the genomic or antisenonic strand of a negative-strand RNA virus; and an activator of RNAse L. The polynucleotide is used to inhibit, or treat, infection by negative-strand RNA viruses, specifically respiratory syncytial virus (RSV) but also (para)influenza, mumps, and rables. The polynucleotide can cross cell membranes without requiring carriers or permeabilizing agents, and can selectively cleave the RNA targeted by the oligonucleotide. The present sequence represents the polynucleotide sequence of RSV strain A2.
                                                                                                                                                                                                                                                                                     10331 CACAAAGTCACACCAACAACTGCAATCATACAAGAATGCAACAAGACCAGATCAAGAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCACAAAACAAACAAACCACCACCAAGCAAACCCAATAATGATTTTCACTTTGAA
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                                                                                                                                                                                      Sequence 15210 BP; 4232 A; 2351 C; 2700 G; 5919 T; 8 other;
                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                             Query Match
91.6%; Score 654.8; DB 20
Best Local Similarity 94.8%; Pred. No. 9.4e-148;
Matches 677; Conservative 0; Mismatches 37;
                 Disclosure; Fig 1; 98pp; English.
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GIGTICAACTITIGIACCCIGCAGCATAIGCAGCAACAAICCAACCCIGCIGGGCIAICIGC
                                                                                                                                                                                                               AAAAGAATACCAAACAAAAACCAGGAAAGAAAACCACTACCAAGCCCACAAAAAACCA
                                                                                                                                                                                                                                                                    CTACTCACCTCCAACACCCACAGGAAATCCAGAACTCACAAGTCAAATGGAAACCTTCCAC
                                                        AAAAGAATACCAAACAAAAAACCAGGAAAGAAAACCACCACCAAGCCTACAAAAAAACCA
                                                                                                                                                                                                                                                  ACCTTCAAGACAACAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
                                                                                                                                                                                                                                                                                                      CTGCTCACCAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                        TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAACTTCCTCCGAAGGCAATCCAAGCCCTTCTCAAGTCTTACAACATCCGAGTACCCA
                                        CAACCCACAAACAGTCAAAACTAAAACACAACAACCAAACAACACAACCCAGCAAGCCC
                                                                                           ACTACAAAACAACCCAAAACCACCAAACAAACCAATAATGATTTTCACTTCGAA
                                                                                                                                               GTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGCTATCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition useful for inhibiting or treating infections against negative-strand RNA virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Torrence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide sequence of RSV strain A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВР
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A human respiratory syncytial virus (RSV) anti-genome sequence (AATG1430) is the 5' to 3' positive-sense sequence of RSV; the genominated is segative-sense. It was synthesised in segments by RT-PCR using intracellular RSV mRNA or genomic rRNA isolated from purified viruses as template. Restriction site markers were introduced by incorporating the changes into the primers used for RT-PCR. The recombinant sequence can be expressed with a nucleocapsid protein, a large polymerase protein and an RNA elongation factor to produce isolated infectious RSV particles useful for generating vaccines against RSV. Recombinant RSV genome or antigenome can also be used as a vector for gene therapy of the AAT63430 standard; DNA; 15223 96WO-US15524. 95US-0007083. (first entry) WPI; 1997-212893/19. 27-SEP-1996; 27-SEP-1995; 03-APR-1997. 02-JUL-1997 Collins PL; Infectious 661 AAT63430; AAT63430
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C RESULT 9 셤 ò 셤 셤 셤 셤 ઠે ठे ò ð 셤 à 5125 ö CACAAAGTCACACCAACAACTGCAATCATACAAGATGCAAGAAGCCAGATCAAGAACACA 4945 ATTACATCACAAATCACCACCATACTAGCTTCAACAACACCAGGGGTCAAGTCAACCTG 5065 5185 180 240 ACTACAAAACAACGCCAAAACAAACCACCAAAACAAAAATGATTTTCACTTCGAA 300 301 GTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGCTATCTGC 360 The present sequence was used in the preparation of a novel polynucleotide, comprising an antisense oligonucleotide, with a polynucleotide, comprising an antisense oligonucleotide, with a tone end, that is complementary to 15-20 bases of the prices, group at one of a respiratory syncytial virus (RSV), a linker attached to the OH-end of the antisense oligonucleotide and an oligonucleotide activator of RNaseL attached to the linker. The polynucleotide can be used to treat RSV infections, which can also be treated by administration of the antisense oligonucleotide, so as to form a complex with activated RNase L in vivo. The polynucleotide can be transported across the cell membranes without carriers or permeability agents, and once introduced destroys antisense target RNA. It also inhibits RSV infection in vitro in a superior manner to the conventional drug, ribavirin. CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGCCAGATCAAGAACACA ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG CAACCCACAACAGTCAAGACTAAAAACACAAACAACCCAAACCCCAGCAAGCCC Gaps Polymucleotide containing sequence anti-sense to region of RSV -connected via a linker to an activator of RNaseL, used to treat RSV Length 15222; ö Sequence 15222 BP; 5923 A; 2706 C; 2356 G; 4237 T; 0 other; 37; Indels Antisense oligonucleotide, respiratory syncytial virus; RSV; treatment; infection; inhibition; strain A2; ss. Xiao DB 18; Pred. No. 9.4e-148; 0; Mismatches 37; Torrence PF, Human respiratory syncytial virus strain A2 91.6%; Score 654.8; 94.8%; Pred. No. 9.4 Disclosure, Pages 47-51, 89pp, English. Human respiratory syncytial virus Cirino NM, Li G, Silverman RH, (CLEV-) CLEVELAND CLINIC FOUND. (USSH) US NAT INST OF HEALTH. 96US-0011725. 97WO-US02531 (first entry) Local Similarity 94.8 les 677; Conservative WPI; 1997-424748/39. 14-FEB-1997; 21-AUG-1997. 17-MAR-1998 infections 9005 9909 Н 4886 62 4946 121 181 241 Query Match Best Loca Matches g à qq 셤 8 g ò 셤 ò ₹

5365 5425 5485 5545 099 480 600 5486 TCAACTICCTCCGAAGGCAATCCAAGCCTTCTCAAGTCTCTACAACATCCGAGTACCCA 5186 GIGITCAACITIGIACCCIGCAGCATAIGCAGCAACAATCCAACCTGCTGGGCTAICTGC 361 AAAAGAATACCAAACAAAAAACCAGGAAAGAAAACCACCACCAAGCCTACAAAAAAACCA 421 ACCTICAAGACAACCAAAAAAGAICTCAAAACCTCAAAACCAAAAGGAAGTACCC 5306 ACCCICAAGACAACCAAAAAAGAICCCAAACCICAAACCACIAAAICAAAGGAAGIACCC 541 CTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAAATGGAAACCTTCCAC 601 TCAACCICCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA Infectious respiratory syncytial virus particles - useful for treatment of RSV or gene therapy of upper respiratory tract diseases RSV; vaccine; gene therapy; upper respiratory tract disease; ss. Human respiratory syncytial virus strain A2 Respiratory syncytial virus anti-genome. (USSH) US DEPT HEALTH & HUMAN SERVICES Claim 46; Page 43-51; 66pp; English. Teng MN

Collins PL, Juhasz K, Murphy BR,

97WO-US12269. 97US-0047634 96US-0021773 97US-0046141

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This is the 5'-3' positive sequence nucleotide sequence of respiratory syncytial virus (RSV) D46. The genome is negative-sense; the complete nucleotide sequence of the negative-sense; the complete nucleotide sequence of the wild-type B-1 virus has also been determined (see AAV1755).

A novel infectious recombinant RSV comprises a RSV genome or antigenome, a major nucleocapsid (N) protein, a nucleocapsid (N) protein, a nucleocapsid (N) antigenome or nucleocapsid (N) protein, a nucleocapsid (N) antigenome or nucleocapsid (N) antigenome or sequence ensitive (Es) substitution at amino acid Phe521, antigenome in the RSV polymerase gene or a ts; nucleotide substitution in the gene-start sequence of gene M2.

Also claimed are: (1) an isolated infectious RSV particle which comprises a recombinant RSV (anti)genome, N, P, and L proteins, a RNA polymerase elongation factor, where the (anti)genome is modified: (1) to ablate or modulate expression of a SH, NS1, NS2 or G gene or a cis-acting regulatory sequence; and (ii) by a termination codon introduced within a selected gene, or by a change in sequence, position or presence of a GS or GE transcription signal relative to the selected gene, (2) an expression vector; and (3) an RSV strain selected from cpts RSV 248 (ATCC WR 2453), cpts RSV 530 (ATCC WR 2452), or cpts 530/1030 (ATCC WR 2451), cpts 248/4955 (ATCC WR 2453), cpts RSV 530 (ATCC WR 2452) or cpts 530/1030 (ATCC WR 2452) or cpts 105/2026 (ATCC WR 2451) or cpts 830/1030 (ATCC WR 2452) or cpts moderned recombinant RSV and RSV particles are used in a vaccine to returned recombinant RSV and RSV particles are used in a vaccine to returned and a system of a mindividual to induce or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expense or expens
                                                                                                                                                                                                                                          Attenuated respiratory syncytial virus vaccines - useful to protect
individuals against RSV infection
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                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES
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Whitehead SS;
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                Sequence 15223 BP; 5921 A; 2704 C; 2361 G; 4236 T; 1 other;
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                                                Query Match 91.6%; Score 654.8; DB 18; Best Local Similarity 94.8%; Pred. No. 9.4e-148; Matches 677; Conservative 0; Mismatches 37;
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                                         Gaps
Score 654.8; DB 19; Length 15223;
Pred. No. 9.4e-148;
0; Mismatches 37; Indels 0; (
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Query Match 91.6%;
Best Local Similarity 94.8%;
Matches 677; Conservative
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RSV; attenuation; vaccine; pneumonia; bronchiolitis; ss.

Human respiratory syncytial virus D46

409802530-A1

22-JAN-1998

Respiratory syncytial virus antigenome

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/note= "creates SphI site in F/M2 intergenic region"
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/note= "creates Stul site in G/F intergenic region"
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/note= "creates StuI site in G/F intergenic region"
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/note= "creates Ncol site in N gene nontranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSV; vaccine; attenuation; pneumonia; bronchiolitis; mutant; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "single C insertion to create AfIII site
  in the NS2-N intergenic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory syncytial virus D46 5'-3' positive sense sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Human respiratory syncytial virus. Chimeric - Bacteriophage 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA88743 standard; cDNA; 15223 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replace (1139, A)
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/*tag= a
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4947 ACCCCAACATACCTCACCCAGAATCCTCAGCTTGGAATCAGTCCCTCTAATCCGTCTGAA 5006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4887 CACAAAGTCACACCAACAACAGCAATCATACAAGATGCAACAAGACCAGATCAAGAACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ACTACAAAACAACGCCAAAACAAACCACCCAAAACCAATAATGATTTTCACTTCGAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of the 5' to 3' positive-sense sequence of human respiratory syncytial virus (RSV); the genome 1861 is negative-sense. This antigenome cDNA, termed D46, was synthesized in segments by RT-PCR using synthetic oligonucleotides as purimers and intracellular RSV mRNA or genome RNA isolated from as purimers and intracellular RSV mRNA or genome RNA isolated from conviral G triplet contributed by the T7 promoter, 4 sequence markers (see AAA88745-47) at positions 1059 (which adds 1 nucleotide contributed to the 3' end by ribozyme cleavage. The invention contributed to the 3' end by ribozyme cleavage. The invention contributed to the 3' end by ribozyme cleavage. The invention cucleocapsid (N) protein, a nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P), a charge polymerase protein (1), an RNA polymerase elongation factor, and a partial or complete RSV genome or antigenome of one RSV errain or subgroup virus. The chimeric RSV is cifferent RSV strain or subgroup virus. The chimeric RSV is ciffered at the unsubsection of selected mutations. It is useful as a vaccine against RSV, which causes classes such as pneumonia and bronchiolitis in infants. The chimeric representation or subgroup virus in an antitype and a partial results RSV infection and attenuated, preferably by introduction of selected immune system of an individual is stimulated to induce protection and individual is stimulated to induce protection of against RNA in a result we made and protection and protection and protection and protection and protection of selected immune system of an individual is stimulated to induce protection and antitype made and protection with a protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and protection and
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                                                                                                                                                                                                                                                                                                                                                 Infectious chimeric respiratory syncytial virus (RSV) produced from cloned nucleotide sequences, useful as a vaccine against diseases caused by the virus, such as pneumonia and bronchiolitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to achieve protection against multiple RSV strains and/or subgroups
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 15223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15223 BP; 5921 A; 2705 C; 2361 G; 4236 T; 0 other;
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                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Page 262-268; 280pp; English.
                                                                                                                                                                                                                                       Collins PL, Murphy BR, Whitehead SS;
                                                                                                                13-APR-1999; 99US-0291894.
                                                        31-MAR-2000; 2000WO-US08802.
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19-0CT-2000.
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ACCCCAACATACCTCACCCAGAATCCTCAGCTTGGAATCAGTCCCTCTAATCCGTCTGAA 121 ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCCAGGAGTCAAGTCAAACCTG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric nucleic acid construct for immunizing animals and humans against respiratory syncytial virus (RSV), comprises a sequence adapted for expression in plants and a RSV protein or peptide coding sequence
CTGCTCACCAACAACACCACAGGAAATCCAAAACTCCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                 CTACTCACCTCCAACACCACAGGAAATCCAGAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                                    TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
                                                                                                                                                                        TCAACTTCCTCCGAAGGCAATCCAAGCCCTTCTCAAGTCTCTACAACATCCGAGTACCCA
                               ACCTTCAAGACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
                                                 ACCCTCAAGACAACCAAAAAGATCCCAAACCTCAAACCACTAAATCAAAGGAAGTACCC
                                                                                                                                                                                                      The present invention relates to a chimeric nucleic acid construct comprising: a nucleotide sequence adapted for protein expression in plants, and a respiratory syncytial virus (RSV) coding sequence encoding an RSV protein or an antigenic protein or peptide of RSV. The construct can be used to immunize animals and humans against respiratory syncytial virus. The use of transgenic plants to generate the antigen allows the production of greater amounts of
                                                                                                                                                                                            Chimeric; respiratory syncytial virus; RSV; immunize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krasnyanski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۵,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 10; 67pp; English
                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sandhu
                                                                                                                                                                                                                                                                 DNA; 918
                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2000; 2000WO-US12582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNII ) UNIV ILLINOIS FOUND
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                           Human RSV G-protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Korban SS,
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                                                                                                                                                                                                                                                                 AAC88494 standard;
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                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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ACCACCAAGCCCACAGAAGAGCCCATCAACAACACAAAACATCATAACTACA

ACCCTCAAGACAACAAAAAGATCCCAAACCTCAAACCACTAAATCAAAGGAAGTACCC

634 481

421

ACCITICAAGACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC

CTACTCACCTCCAACACCACAGGAAATCCAGAACTCACAAAGTCAAATGGAAACCTTCCAC

754

601 814 199

541

TCAACTICCTCCGAAGGCAATCCAAGCCCTTCTCAAGTCTCTACAACATCCGAGTACCCA

TCACAACCCTCATCTCCACCCAACACACACGCCAGTAGTTATT 874 TCACAACCTTCATCTCCACCCCAACACACCACCCCAGTAGTTACT

917 704

TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA

CTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC

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antiviral;
                                                                                                       RSV; ds; G protein; heavily glycosylated protein; antianaemic; vaccine; gene therapy; paramyxovirus; sendai virus; PWV; antiviral chemotherapeutic compound; humoral response; cellular immune response; hPIV; paediatric respiratory disease; globin gene transfer; sickle cell disease; beta-thalassaemia; human immunodeficiency virus infection; HIV.
                                                                               Respiratory syncytial virus G protein DNA.
                                                                                                                                                                                                                                                                       protein"
                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                       respiratory syncytial virus
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AAS20145 standard; DNA; 897
                                                    (first entry)
                                                                                                                                                                                                                                                         /*tag= a
/product=
                                                                                                                                                                                                                                              ..897
                                                    09-APR-2002
                          AAS20145;
                                                                                                                                                                                                     Human
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Gaps

Score 649.6; DB 22; Length 918; Pred. No. 8.1e-147; 0; Mismatches 34; Indels 0;

Query Match
Best Local Similarity 95.2%;
Matches 670; Conservative

Sequence 918 BP; 366 A; 293 C; 100 G; 159 T; 0 other;

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(UYAL-) UNIV ALABAMA.
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                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a recombinant Sendar virus comprising an antigenic fragment. The virus may be administered in combination with an antifytral chemotherapeutic compound. Two or more viruses expressing different PMV proteins nay be co-administered. Compositions comprising the virus are useful for eliciting a humoral and/or cellular immune response to a PMV in a mammal, particularly a human. Further a recombinant Sendai virus comprising an exogenous moleic acid encoding a second PMV protein is also administered and priming and/or controling a second PMV protein is also administered and priming and/or posting humoral or cellular immune response comprises administering one or more of a recombinant or isolated PMV protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendai viral vector encoding a PMV protein. The recombinant virus is useful as an effective vaccine against hPIV or RSV (the major causes of paediatric respiratory disease) and also to express any gene of interest in target cells, providing a positive medical impact on impaired cells #Mild-type globin gene transfer (i.e. gene therapy) into stem cells effects a cure for sickle cell disease or betathassaemia. The recombinant virus may also prove effective in conferring immunity to human immunodeficiency virus (HIV) infection. The Sendai virus replicates at level that is high enough to induce sufficient immunity, but does not cause any harm to human virus (RSV) g protein (heavily glycosylated protein), a PMV protein virus suitable for expression by the recombinant virus of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 ACCACBARACBACGCCBARACBARCCCCCARGCBARCCCARTRATGATTTTCACTTTGAR 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGAGCCAGATCAAGAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 CACAAAGTCACCAACAACTGCAATCATACAAGATGCAACAAGCCAGATCAAGAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 ACCCCAACATACCTCACCAGAATCCTCAGCTTGGAATCAGTCCCTCTAATCCGTCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 ACTACAAAACAAGGCGAAAACAAACCACCAAACAAACCAATAATGATTTTGACTTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAACCCACACAGTCAAGACTAAAACACAACAACAACCCAAACACAACCCAGCAAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAATCCACAACAGTCAAAGACCAAAAACACAACAACAACTCAAACACAACCCAGCAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                           Recombinant Sendai virus useful in vaccines to protect infection by paramyxoviruses, comprises exogenous nucleic acid encoding paramyxovirus protein or its antigenic fragment
                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a recombinant Sendai virus comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
90.4%; Score 646.2; DB 24; Length 897;
Best Local Similarity 95.3%; Pred. No. 5.3e-146;
Matches 666; Conservative 0; Mismatches 33; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 897 BP; 359 A; 289 C; 95 G; 154 T; 0 other;
                                                                                                                                                       (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 47; 57pp; English.
                                                                                 22-MAY-2001; 2001WO-US16610.
                                                                                                                    01-JUN-2000; 2000US-208701P.
                                                                                                                                                                                      Portner A, Takimoto T;
                                                                                                                                                                                                                        WPI; 2002-130534/17.
                                                                                                                                                                                                                                          P-PSDB; AAU74676.
                WO200192548-A2.
                                                  06-DEC-2001.
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301 GIGTTTAACTTTGTACCCTGCAGCATATGCAACAACCAACCTGCTGGGTTATCTGC 360
                                  499 GIGITICAACTITGIACCCIGCAGCAIAIGCAACCAACCAACCIGCIGCIGGGCTATCIGC 558
                                                                                                                                          420
                                                                                                                                                                                                                   618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            738
                                                                                                                                                                                                                                                                                                                                                                                                                                   739 CTACTCACCTCCAACACCACAGGAAATCCAGAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCCACAACATCCGAGCACCCA
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                                                                                                                                                                                                                                                                                     421 ACCTTCAAGACAACCAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
                                                                                                                                                                                                                                                                                                                                                      619 ACCCICAAGACAACCAAAAAGAICCCAAACCICAAACCACIAAAICAAAGGAAGIACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 CTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSV; glycoprotein G; pneumococcal surface protein A; PspA;
infection; Streptococcus pneumoniae; sepsis; otitis media;
meningitis; bacteraemia; pneumonia; vaccine; genetic immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Respiratory syncytial virus glycoprotein G gene portion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 TCACAACCCTCATCTCCACCCAACACACACGCCAGTAG 699
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membrane where it can be exposed to the host immune system.

C Insertion of pneumococcal surface protein A (PBpA) coding sequence created plasmid pKSD2601. Intramuscular immunisation of BALBA/C mice with pKSD2601 induced protection against an otherwise lethal cohallenge with a capsular type 3 pneumococcus. A claimed plasmid for expression of pneumococcal epitope DNA in enkaryotic cells includes a promoter for driving expression in a eukaryotic cells includes a promoter for driving expression in a eukaryotic cells (e.g. HCMV-IE), DNA encoding a leader sequence (e.g. of RSVG) cand DNA encoding a pneumonoccal epitope such as PspA. The invention also provides a vaccine comprising the plasmid and a suitable carrier or diluent, and optionally one or more cytokines or DNA encoding them, or a bacterial delivery system. The vaccine is used to elicit an immunological response in a host, including humans, susceptible to pneumococcal infection or sepsis. The plasmid can also be used to express a pneumococcal epitope of interest in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 696 BP; 284 A; 211 C; 78 G; 123 T; 0 other;
      8$888888888888888
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Attenuated respiratory syncytial virus vaccines - useful to protect individuals against RSV infection

Example 4; Page 195-202; 238pp; English

Teng MN;

Juhasz K, Murphy BR,

(USSH) US DEPT HEALTH & HUMAN SERVICES

Collins PL,

Bukreyev AA, Whitehead SS;

WPI; 1998-110579/10.

97WO-US12269. 97US-0047634 96US-0021773 97US-0046141

15-JUL-1997; 23-MAY-1997; 09-MAY-1997;

.5-JUL-1996;

WO9802530-A1

22-JAN-1998

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                                                                                     121 ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCCAGGAGTCAAGTCAAACCTG
                                                                                                                                                                             CAACCCACAACAGTCAAGACTAAAAACACAAAC-AACCCAAACACAACCAGCAAGCC
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                        Gaps
                       1;
DB 19; Length 696;
Score 445.8; DB 19; Length
Pred. No. 8.4e-98;
0; Mismatches 22; Indels
Query Match
Best Local Similarity 95.3%;
Matches 470; Conservative
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5008 ACCACATCACAATCCACACAAATTCAGCCACAACATCACCCAACACAAAGTCAGAAACA 5067
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A novel infectious recombinant RSV comprises a RSV genome or antigenome, a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P), a large polymerase protein (L), and a RNA polymerase elongation factor, where the recombinant RSV has at least two attenuating mutations, one of the mutations specifying a temperature-sensitive (ES) substitution at amino acid Rhe521, and claimed are: (1) an isolated infectious RSV particle which comprises a recombinant RSV (anti)genome, N, P, and L proteins.

Comprises a recombinant RSV (anti)genome, N, P, and L proteins, RNA polymerase elongation factor, where the (anti)genome is modified: (1) to ablate or modulate expression of a SH, NS1, NS2 or G gene or introduced within a selected gene, or by a change in sequence, position or presence of a GS or GB transcription signal relative to the selected gene, (2) an expression vector; and (3) an RSV strain selected from cpts RSV 248 (ATCC WR 2450), opts 248/404 (ATCC WR 2452), cpts 830/1009 (ATCC WR 2451), cpts 844/40 (ATCC WR 2452), cpts 830/1009 (ATCC WR 2451) or cpts 530/1009 (ATCC WR 2451) or cpts 530/1009 (ATCC WR 2452) or entimalate prenamentary and RSV particles are used in a vaccine attenuated recombinant RSV and RSV particles are used in a vaccine of entimalate prenamentary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CHACCCACACCACAGACTAAAAACACAACAACAACCAAACACACAACCAAGCCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ACTACAAAACAACGCCAAAACAAACCACCAAAACAAACCAAATAATGATTTTTCACTTCGAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CACAAAGICACTAACAACTGCAATCATACAAGATGCAACAAGACCAGATCAAGAACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protection against RSV. The expression vector of (2) the production of infectious attenuated RSV particles.
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RSV; attenuation; vaccine; pneumonia; bronchiolitis; ss.

syncytial virus genome.

(first entry)

20-JUL-1998

AAV17552;

AAV17552 standard; cDNA; 15225 BP.

Human respiratory syncytial virus B-1

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5128 AGCACAAAACCACGTAAAAAATCCACCAAAAAAACCAAAAAAGTGATTACCATTTTGAA 5187
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                                                                                                             538 ACACTGCTCACCAACAACACCACAGAAATCCAAAACTCACAAGTCAAATGGAAACTTC 597
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Search completed: October 29, 2003, 22:09:35 Job time : 246.018 secs

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GenCore version 5.1.6
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OM nucleic - nuc	nucleic search, using sw model
Run on:	October 29, 2003, 16:51:32 ; Search time 2923.85 Seconds (without alignments) 10004.074 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-462-816-3 715 1 cacaaagtcacactaacaacgtagttattaaaaaaaaa 715
Scoring table:	IDENTITY NUC Gapop 10-0 , Gapext 1.0
Searched:	2888711 segs, 20454813386 residues
Total number of	hits satisfying chosen parameters: 5777422
Minimum DB seq] Maximum DB seq]	length: 0 length: 2000000000
Post-processing:	: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	### ### ##############################

41: em_ntgo_otner:* Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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	715	100.0	920		A16258	nthetic
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	715		920		AR122885	AR122885 Seguence
	715		920		AR123540	Sequenc
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	8.4	91.6	15223	۲	AR089137	ARORGIAT Semience
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	9.0	87.9	840	4	AF193308	AP10220g Human mon
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	621	86.9	922	14	HRSCVGC	Z33456 Human respi
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	621	86.9	922	14	HRSVGL12	Z33425 Human resp.
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	7.8	86.4	922	14	AF065256	AF065256 Human res
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		86.4	922	14	HRSVGL9	Z33422 Human respi
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RESULT 1 RD081934						
Locus	BD08	4			715 bp DNA	linear PAT 27-AUG-20
DEFINITION	Nucleic		cid vaccines	ines	3 protein	respirat
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VERSION	BD08	1934.1	81934.1 GI:2262	75	44	
SOURCE	Resp	uulsiz irator	662-A/2 V SVNCV		airin	
ORGANISM	Resp	irator	Respiratory syncytial	tial		
	Viru	Viruses; s Paramyxovi	Viruses; ssRNA nega Paramyxoviridae; Pn	gati Pneu	ssRNA negative-strand viruses; Mon viridae; Pneumovirinae; Pneumovirus	Mononegavirales; rus,
KEFERENCE AUTHORS	ri.	bases ., Sam	es 1 to 719 Sambhara, S	an	and Klein.M.H.	
TITLE	Nucl	eic acid	id vaccines	ines	ing G protein	of respiratory syncytial

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03-OCT-1994

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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/db_xref="taxon:12814"
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Patent: JP 2001512662-A 2 28-AUG-2001,
CONNAUGHT LABORATORIES LTD
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/mol_type="genomic DNA"
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Synthetic RSV G gene (seq ID No: 7).
A16258
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Location/Qualifiers
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Klain, W.H., Du, R.-E. and Bwasyshyn, M.E.
Multimeric hybrid gene encoding a chimeric protein which confers
protection against parainfluenza virus and respiratory syncytial
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	RESULT 6	Query Match 100.0%; Score 715; DB 6; Length 920; Best Local Similarity 100.0%; Pred. No. 3.3e-151; Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 CACADAGTCACATACACATCATACAAGTGCAACAAGCCAGATCAAGAACACA Db 206 CACAAGTTCACACTACAACATCATACAAGATGCAACAAGCCAGATCAAGAACACA CACCCAACATACCTCACTCAGATCATACAAGATGCAACAAGCCAGATCAAGAACACAAGAACAACAACAACAACAACAACAACAACA
421 ACCTTCAAGACAACCAAAAAGATCTCAAACCTCAAACCTAAACCAAAGGAAGTACCC 480 626 ACCTTCAAGACCACCAAAAAAGATCTCAAACCTCAAACCAAAACGAAGGAAG	AR092530 AR092530 BETINITION AR092530 AR09263 AR09	Query Match 100.0%; Score 715; DB 6; Length 920; Best Local Similarity 100.0%; Pred. No. 3.3e-151; Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY 1 CaCaaaGTCACACTAACAACACACAACAACAACAACACAAC

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	421 ACCTTCAAGACAAAAAAGATCTCAAACCTCAAACCTAAAACCAAAGGAAGTACCC 	481 ACCACCAAGCCCACAGAAGACCAACCATCAACACCACCAAAACAAAC	541 CTGCTCACCAACAACACACAGAAATCCAAAACTCAAAGTCAAATGGAAACCTTCCAC 	601 TCAACCTCCGGAAGGAATCTAAGCCTTCTCAAGTCTCCACAACATCCGAGCACCCA	661 TCACAACCTCATCTCCACCCAACACACACCCCGGTAGTTATTAAAAAAAA	AR123540 920 bp DNA linear PAT 16-MAY Sequence 7 from patent US 6171783. AR123540 AR123540 Unknown.	Unclassified. 1 (bases 1 to 920) Klein,M.H., Du,RP. and Ewasyshyn,M.E. Infection detection method using chimeric protein Patent: US 6171783-A 7 09-JAN-2001;	1920 /organism="unknown" 380 a 290 c 95 g 155 t	100.0%; Score 715; DB 6; Length 920; imilarity 100.0%; Pred. No. 3.3e-151;	Matches /15; Conservative 0; Mismatches 0; Indels 0; Gaps / CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGCAGATCAAGAACACA	206 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGAGCCAGATCAAGAACACA 61 ACCCCAACATACCTCAACACTCAGGATCCTCAGGTTGGAATCAGCTTGGAATCAGCTTGGAATCAGCTTGTAAA	266 ACCCCAACATACTCAGTTCTCAGCTTGGAATCAGCTTCTCAATCTGTAA 121 ATTACATCACAAACCACCACCACCATCTAGCTTCTAACAACACCAAGAGTCAAGTCAAACTG	326 ATTACATCACAAACCACCACCATACCTTCAACAACACCAGGAGTCAAGTTCAAACCTG	181 CAACCCACAACAGTCAAGACTAAAACACAACAACAACCCAAACACAAGACACGGAAGCCC 386 CAACCCACAACAGTCAAGACTAAAAACACAACAACAAACA	ACTACAAAACAACGCCAAAACCACCCAAACAAACCAAAC	ACIALAMAAGCAGCGAMAACAACCACCAAACAAACAATAATGATTTTCACTTCGAA GTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGCTATCTGC	

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/db_xref="SPTREMBL:Q01929"
/tale1ation="MSKNEDGRIAKTLEKTWDTLAVILETSSGLYKLNLKSIAQITLS
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NLSEITSGTTTILASITERSAHEVYLLTTTGTGPSKPTTKQRGNKPPNKPN
NDEPREVPROVOCSICSNNPTCWAICKRIPNKKPTTKPTROTGPSKPTTKKDLKPO
NDFREVPTTKPTREPERPINUTTKTNITTTLINNTTGNPKLTSGNRTFHSTSSEGNLSP
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100.0%; Pred. No. 4.4e-150;
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HRSVGL16 922 bp RNA linear VRL 05-JUN-1997
Human respiratory syncytial virus (MON-7-91) subgroup A, G gene for g1ycoprotein.
233429.
G gene, G1:485888
G gene, Glycoprotein.
Human respiratory syncytial virus
Human respiratory syncytial virus

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS DEFINITION

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Direct Submission
Submitted (10-MAY-1994) Dopazo J., Centro Nacional de Biotecnologia
- CSIC, BioInformatica, Universidad Autonoma, Cantoblanco, Madrid, SPAIN, 28049
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                                                                                   Evolutionary pattern of human respiratory syncytial virus A): cocirculating lineages and correlation of genetic and changes in the G glycoprotein J. Virol. 68 (9), 5448-5459 (1994)
Viruses; ssRNA negative-strand viruses; Mononegavirales; Baramyxoviridae; Pneumovirinae; Pneumovirus. 1 (bases 1 to 922) darcia, O., Martin, M., Dopazo, J., Arbiza, J., Fabrasile, S., Hortal, M., Perez-Brena, P., Martinez, I., Garcia-Barreno, B.
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/organism="Human respiratory syncytial virus"
/mol_type="genomic RNA"
/mol_type="genomic RNA"
/isclate="MON 7 91 (Montevideo/Uruguay, 1991)"
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/cill_line="HEp-2"
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Location/Qualifiers
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attachment glycoprotein; surface glycoprotein.
Human respiratory syncytial virus
Human respiratory syncytial virus
Mytuses; seRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.

B. (bases 1 to 917)
S. Johnson, P.R., Spriggs, M.K., Olmsted, R.A. and Collins, P.L.
The G glycoprotein of human respiratory syncytial viruses of subgroups A and B: extensive sequence divergence between antigoenically related proteins
E. Proc. Natl. Acad. Sci. U.S.A. 84 (16), 5625-5629 (1987)
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    917 — Paramer Lespiratory syncytial virus"
/organism="Human respiratory syncytial virus"
/nol_type="genomic RNA"
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Pred. No. 1.2e-147;
0; Mismatches 3;
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/note="attachement glycoprotein
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Klein,M.H., Du,R.-P. and Ewasyshyn,M.E.
Multimeric hybrid gene encoding a chimeric
protection against parainfluenza virus and
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97.3%; Score 696; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 6.4e-147;
Matches 696; Conservative 0; Mismatches 0;
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Sequence 28 from patent US 5968776.
AR080424.1 GI:10007159
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Location/Qualifiers
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REHICE

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Human respiratory syncytial virus nonetructural protein (1C),

nonstructural protein (1B), major nucleocapsid (N), phosphoprotein (P), protein (M), 1A, 0 (G), protein (P) and

envelope-associated protein (22K) gene, complete cds.

MI1486 K01459 K03719 K03348 K03349 MI1217 MI1244 MI1487 MI1505

MI1546 MI1631 MI2056

MI1646 I GT:333025

S michecapsid protein; fusion glycoprotein; major nucleocapsid protein; major surface glycoprotein; major nonstructural protein; phosphoprotein.

Human respiratory syncytial virus

Human respiratory syncytial virus

Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.

CE 1 (bases 1085 to 2220; 5254 to 5544)

Blango, N. and Verkategan, S.

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Nucleic Acids Res. 11 (17), 5941-5951 (1983)
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Klein, M.H., Du, R.-P. and Ewasyshyn, M.E.
Multimeric hybrid gene encoding a chimeric protein which confers
protection against parainfluenza virus and respiratory syncytial
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Seguence 28 from patent US 5998169.
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Satake,M., Elango,N. and Venkatesan,S.
Sequence analysis of the respiratory syncytial virus phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins, P.L. and Wertz, G.W.
The envelope-associated 22K protein of human respiratory syncytial virus: nucleotide sequence of the mRNA and a related polytranscript J. Virol. 54 (1), 65-71 (1985)
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Satake, M., Coligan, J.B., Elango, N., Norrby, E. and Venkatesan, S.
Respiratory syncytial virus envelope glycoprotein (G) has a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   syncytial virus reveals an unusual type of viral membrane protein
Proc. Natl. Acad. Sci. U.S.A. 82 (12), 4075-4079 (1985)
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Collins, P.L. and Wertz, G.W.
Nucleotide sequences of the 1B and 1C nonstructural protein mRNAs of human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding
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                                                     Satake, M. and Venkatesan, S.
Nucleotide sequence of the gene encoding respiratory syncytial
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Wertz,G.W., Collins,P.L., Huang,Y., Gruber,C., Levine,S. and
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Elango, N., Satake, M., Coligan, J.E., Norrby, E., Camargo, E.
Venkatesan, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 (bases 8 to 1050; 7554 to 8506).
Blango,N., Satake,M. and Venkatesan,S.
mRNA sequence of three respiratory syncytial virus genes two nonstructural proteins and a 22K structural protein J. Virol. 55 (1), 101-110 (1985)
                                                                                                                                                                                                                                                                                                          4 (bases 5602 to 7500)
Collins, P.L., Huang, Y.T. and Wertz, G.W.
Nucleotide sequence of the gene encoding the fusion (F)
glycoprotein of human respiratory syncytial virus
Proc. Natl. Acad. Sci. U.S.A. 81 (24), 7683-7687 (1984)
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                                                                                             virus matrix protein
J. Virol. 50 (1), 92-99 (1984)
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Collins, P.L. and Wertz, G.W.
The 1A protein gene of humar
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13 (bases 1051 to 1080, 2278 to 2287, 3192 to 3210, 4158 to 4172, 4572 to 4626; 5545 to 5601; 7501 to 7578)
Collins,P.L., Dickens,L.E., Buckler-White,A., Olmsted,R.A., Spriggs,M.K., Camargo,E. and Collingh,K.V.
Nucleotide sequences for the gene junctions of human respiratory syncytial virus reveal distinctive features of intergenic structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reprint for [2] and clean copy sequence for [12], [5] kindly provided by P.Collins, 21-FEB-1986.
Respiratory syncytical virus is a negative-strand RNA pleomorphic enveloped virus of the genus Pneumovirus. The matrix protein has no homology with the matrix proteins of other negative-stranded RNA viruses, implying that RS virus has undergone extensive evolutionary divergence. Two unidentified reading frames which potentially encode proteins were located: one overlaps the matrix protein and the other the P protein. The biological significance of these two reading frames is not clear. The positive strand is
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VIHTIKLNGIVFVHVITSSDICPNNNIVVKSNFTTMPVLQNGGYIWEMMELTHCSQPN
GLLDDNCEIKFSKKLSDSTWTNYMNQLSELLGFDLNP"
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HECIVRKLDEKQATFTFLVNYEMKLLHKVGSTKYXKYTEYNTKYGTFPMPIFINHDGF
LECIGIKPTKHTPIIYKYDLNP"
12 (bases 1081 to 2277)
Collins, P. L., Anderson, K., Langer, S.J. and Wertz, G.W.
Correct sequence for the major nucleocapsid protein mRNA respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 83 (13), 4594-4598 (1986)
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/replace="g"
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'protein id="AAB59850.1"
'db_xref="G1:333926"
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/lab_host="HEp-2 cell"
                                                                                                                 Virology 146 (1), 69-77 (1985)
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/gene="1B"
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/protein_id="AAB59852.1"
/db_xref="G1:333928"
        in [6]
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/product="phosphoprotein"
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/gene="N"
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Listing first 45 summaries
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127 QPITVKIKNITITIQIQPSKPITKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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InterPro; IPR000925; Glycoprot G.
InterPro; IPR006162; Ppantue attach.
Pram, PF08082; Glycoprotein G; 1.
PROSITE; P800012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 298 AA; 32771 MW; FRCD4213D97C2952 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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67 HKVTLTTAIIQDATSQIKNTTPTYLTQNPQLGISFSNLSETTSQTTTLLASTTPSVKSTL 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of mutations contributing to the reduced virulence of a modified strain of respiratory syncytial virus."; Vaccine 14:1637-1646(1996).
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR00925; Glycoprot G.
InterPro; IPR008625; Ppatne_attach.
Pfam; PP00802; Glycoprotein G; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 298 AA; 32779 MW; 67F4A043682FA450 CRC64;
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01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
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Paramyxoviridae; Pneumovirinae; Pneumovirus
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MEDLINE=97185152; PubMed=9032893;
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Matches 209; Conservative
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                                                      NCBI TaxID=12814;
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Choi E.H., Lee H.J.;

"Generic diversity and molecular epidemiology of the G protein of

subgroups A and B of respiratory syncytial virus isolated over 9

consecutive epidemics in Korea.";

J. Infect. Dis. 181:1547-1556 (2000).
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                                                                                             Query Match 88.9%; Score 1093; DB 12; Length 299; Best Local Similarity 90.1%; Pred. No. 1.9e-78; Matches 209; Conservative 6; Mismatches 17; Indels 0;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
           InterPro; IPR000925; Glycoprot_G.
InterPro; IPR006162; Ppantine attach.
Pfam; PF00802; Glycoprotein G; 1.
PROSTITE; PS00012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 298 AA; 32749 MW; 60F27B29D4997F31 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Glycoprotein (Fragment).
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EMBL; U39662; AAC57026.1; -.
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Best Local Similarity
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SEQUENCE
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48 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSETTSQTTTILASTTPSVESTL 107
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J. Infect. Dis. 181:1547-1556 (2000).

EMBL, AF193306; AAF23729.1; -.
InterPro; IPR000925; Glycoprot_G.
                          228 LITHNITGNPEHTSQKETLHSTSSEGNPSPSQVYTTSRYLSQPPSPSNTTNQ 279
181 LLINNTIGNPKLISQMETFHSISSEGNLSPSQVSITISEHPSQPSSPPNTTRQ 232
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Human respiratory syncytial virus.
Viruses; sEMAn negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
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MEDLINE=20283719; PubMed=10823752;
Choi E.H., Lee H.J.;
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MEDLINE=99022964; PubMed=9806017;
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KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKGVPTTKPTEBPTINTTKTNITT 180
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MEDLINE=99022964; PubMed=9806017;
MEDLINE=99022964; PubMed=9806017;
Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
"Antigenic and genetic diversity among the attachment proteins of
group A respiratory syncytial viruses that have caused repeat
infections in children.";
J. Infect. Dis., 178:925-932 (1998).
EMBL; AF065407; AAD02943.1;
InterPro; IPR000225; Glycoprot G.
InterPro; IPR000225; Glycoprot G.
InterPro; IPR006162; Ppantne attach.
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                                                                                                                                                                                                                                                                                              247 LLTSNTTRNPELTSQMETFHSTSSEGNPSPSQVSITSEYPSQPSPPNTSR 297
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01-MAR-2003 (TEMBLEL). 23, Last amnotation update)
Attachment glycoprotein G (Fragment)
Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Best Local Similarity 88.8%; Pred. No. 4.3e-76;
Matches 206; Conservative 6; Mismatches 20
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MEDLINE=94335057; PubMed=8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Garcia O., Martin B., Martinez I., Garcia-Barreno B.,
Melero J.A.;
Melero J.A.;
"Evolutionary pattern of human respiratory syncytial virus (subgroup A): cocirculating lineages and correlation of genetic and antigenic J. virol. 68:5448-5459(1994).

EMBL; Z33427; CAA83870.1; -
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Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.,
"Antigenic and genetic diversity among the attachment proteins of
incorporate and genetic diversity among the attachment proteins of
infections in children...,
J. Infect. Dis. 178.925-932(1998).
EMBL, AF065405; AAD02941.01.
InterPro; IPR000925; Glycoprot. G.
InterPro; IPR000925; Glycoprot. G.
InterPro; IPR006162; Ppantne attach.
Fram; PF008012; PROSTCEIN G.; I.
FROSITE; PS000012; PROSTCEIN G.; I.
SEQUENCE 297 AA; 32572 MW; 5C10E719A05EF5C1 CRC64;
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InterPro; IPR065162; Ppantne attach.
Pfam; PF00802; Glycoprotein G.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 297 AA; 32589 MW; F210F8C68193F5DD CRC64;
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Last annotation update)
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88.7%; Pred. No. 2.1e-76;
iive 7; Mismatches 19
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Matches 205; Conservative
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ö 61 OPTIVKIKNITITOTOPSKPITKORONKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALC 120 180 121 181 241 9 1 HKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTLLASTTPGVKSNL 62 HKVTSTTTIIQDATSQIKNTTPTYLTQNPQLGISPSKPSEITSQITTILASTTPGVKSTL 121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTERPTINTTKTNITTT Gaps 232 ő 181 LLINNITGNPKLISOMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTRQ DB 12; Length 293; 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Attachment glycoprotein G.
Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus. us-09-462-816-4.rspt

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108 OSTIVKTKKTTTTQIQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 167
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   1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSBITSQTTTILASTTPGVKSNL
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"Genetic diversity and molecular epidemiology of the G protein of Subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556 (2000).

EMBL; AF193313; AAF23736.1;
InterPro; IPR000925; Glycoprot G.
InterPro; IPR0001025; Ppantne attach.
Pfam; PP00802; Glycoprotein G; 1.
Prosyne: PROSYIE: PROSPHOPANTETHEINE; 1.
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Viruses, ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
VCBI_TaxID=11250;
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MEDLINE=20283719; PubMed=10823752;
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                                                                    E STRAIN=WUS222;

XX MEDLINE=99022964; PubMed=9806017;

XA SUllender W.W., Museon M.A., Prince G., Anderson L.J., Wertz G.W.;

XA Sullender W.W., Museon M.A., Prince G., Anderson L.J., Wertz G.W.;

XA Sullender W.W., Museon M.A., Prince G., Anderson L.J., Wertz G.W.;

XA Tatigenic and genetic diversity among the attachment proteins of RT group A respiratory syncytial viruses that have caused repeat

RT group A respiratory syncytial viruses that have caused repeat

Infections in children.";

RE MRL, AF065406; AAD02942.1; -.

DR EMBL, AF065406; AAD02942.1; -.

DR InterPro; IPR001025; Glycoprot G.

DR InterPro; IPR001025; Ppantine affrach.

DR Pfam, PF00802; Glycoprotein G; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.

SQ SEQUENCE 298 AA; 32781 MW; ABTC9E05547C5745 CRC64;
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J. Virol. 68:5448-5459(1994).
EMBL. 2343-23, CARASI875.1;
InterPro; IPR000925; Glycoprot_G.
InterPro; IPR0006162; Pantne_attach.
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MEDLINE=94335057; PubMed=8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
Melero J.A.;
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Paramyxoviridae, Pneumovirinae, Pneumovirus.
NCBI_TaxID=11250,
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Last annotation update)
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PROSITE; PS00012; PHOSPHOPANTETHEINE; 1
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Jurol. 68:548-5459(1994).
EMBL; Z33456; CAA83879.1; -.
                                                                                                                                           Mallender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
"Antigenic and genetic diversity among the attachment proteins of
group A respiratory syncytial viruses that have caused repeat
infections in children."

J. Infect. Dis. 178:925-932(1998).

BMID., APG65408; AAAD02944.1;
InterPro; IPR0006162; Ppantne attach.
InterPro; IPR000655; Glycoprot G.
InterPro; IPR000565; Prich extens.
PEam; PP00802; Glycoproted.
PEam; PP00802; Glycoproted.
RINTS; PR01217; PRICHEXTENSN.
PROSTE: PR001217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-subgroup A;
MEDLINE=94335057; PubMed=8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 LLTSNTTRNPELISQMETFHSTSSEGNPSPSQVSITSBYPSQPSSPRNTR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 LLINNTIGNPKLISQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTR 231
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                                                                                                                                                                                                                                                                                                                                         85.7%; Score 1053; DB 12; Length 292; 87.9%; Pred. No. 2.6e-75; ive 8; Mismatches 20; Indels 0.
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Attachment glycoprotein G (Fragment)
Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
VCBI_TaxID=11250;
                                                                                                                                                                                                                                                                                                             SEQUENCE 292 AA; 31964 MW; 8942A8DD0A402A4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) (MAD-1-89) subgroup A, G glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel, 01, Created)
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                                                                                                                                    MEDLINE=99022964; PubMed=9806017;
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                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 87.9
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                       STRAIN=WV19983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT
                                                                                                                                                                                                                                                 1 HKVTLITALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                                                                                                                                                                                            61 QPTIVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 OPTIVKTKNITITIQIQPSKPITKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC
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MEDLINE=9134005; PubMed-1895054;
MEDLINE=9134005; PubMed-1895054;
MIDDLINE=9134005; PubMed-1895054;
MIDDLINE=9134005; PubMed-1895054;
MIDDLINE=9134000 Of Variable domains of the attachment (G) protein of subgroup A respiatory syncytial vuruses.";
J. Gen. Virol. 72:2091-2096(1991).
                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 LLTINITGNPEHTNQRETLASTSSEGNISPSQVYTISEYLSQSPSPSNTT 296
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                                                                                                                                                 Length 297;
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                                                                                                                                      Query Match 85.7%; Score 1053; DB 12; Length Best Local Similarity 87.4%; Pred. No. 2.7e-75; Matches 201; Conservative 8; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Respiratory syncytial virus.
Viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=12814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=RSB99-6256;
Cane P.A.;
Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; X73353; CAA51764.1; -.
InterPro; IPR006925; Glycoprot G.
InterPro; IPR006162; Papatine attach.
Pfam; PP00802; Glycoprotein G; 1.
PROSTIE; PS00012; PHOSPHOPANTETHBINE; 1.
InterPro; IPR006162; Ppantne attach. Pfam; PF00802; Glycoprotein \overline{G}_{i} 1. PROSITE; PS00012; PHOSPHOPANTETHEINE; 1. SEQUENCE 297 AA; 32741 MH; 0E567A174BF64964 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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- 185 KRIPNKKPGKKTTTKPTKKPTIKTTKKDLKPQTTKPKEVLTTKPTEKPTINTTRTNIRTT 244
- 유 **상** 유

Search completed: October 29, 2003, 17:40:53 Job time : 55.717 sec8

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: October 29, 2003, 17:12:25; Search time 12.6943 Seconds

(without alignments) 859.454 Million cell updates/sec

Title: US-09-462-816-4 Perfect score: 1229

Sequence: 1 HKVTLTTAIIQDATSQIKNT......VSTTSEHPSQPSSPPNTTRQ 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	human	3 human	human	2 human	P27026 human respi	P27023 human respi	human	human	P23041 human respi	w	drosc	~	~	xenop	_		m		bovine	7 bovine	5 bovine	sacchar	Q65706 bovine resp			Pl3728 drosophila			O09495 bovine resp	bovine	3 homo	46	s rattu
SUMMAKIES		di.	VGLG HRSVL	VGLG HRSVA	VGLG HRSV6	VGLG HRSV3	VGLG HRSV7	VGLG_HRSV4	VGLG_HRSV5	VGLG HRSV2	VGLG HRSV8	VGLG HRSV1	SGS3 DROME	ZAN HUMAN	MUC2 HUMAN	MUC1 XENLA	SGS3_DROSI	DAN4 YEAST	VGLG_BRSV1	VGLG_BRSV4	VGLG BRSVC	VGLG BRSVW	VGLG_BRSV2	AMYH_YEAST	VGLG_BRSV7	ZAN RABIT		SGS3_DROYA	VGLG ORSVW	VGLG_BRSVS	VGLG BRSVL	VGLG BRSVR	MUSA_HUMAN	MUSB HUMAN	MUC2_RAT
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æ	Query	Match	98.9	91.1	85.6	85.0	84.4	84.1	82.9	82.1	41.1	40.4	16.4	16.2	'n.	S.	4.	4.	4.	•	14.4		13.9		٠	13.5		•	•	٠	•	•	12.5	12.5	12.2
		Score	1216	1120	1052	1045	1037	1033	1019	1009	505.5	497	202	198.5	193	191	183	183	180.5	179.5	177	176.5	170.5	169.5	169	166	164.5	16		159	S.	154	in	153.5	150.5
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	P03200 epstein-bar P54197 coccidioide O88799 mus musculu			
YS89_CAERL VGLX_HSVEB	VGP3_EBV CHI2_COCPO ZAN_MOUSE	ALS1_CANAL VGP3_EBVA8 YOU3_CAEEL	MUA1 XENLA AMYH SACDI P60 LISIN	VGP_MABVM
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3178	907 860 5376	1260 886 1240	400 767 467	681
12.2	12.0 11.0 11.8	11.8	4.11.	11.2
150	147.5 147 145.5	144.5 143 141	139.5 139 138	137.5
35	34 34 38	39 40 41	4 4 4	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                antigenically related professions."

Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).

-!- FUNCTION: VALIES PARAMYSOVIRUS ATTACHBENT PROTEINS, THE STREAMYSOVIRUS ATTACHBENT PROTEINS, THE HEMAGGIUTINATING ACTIVITIES.

-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURRACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

-!- PTM: MAY CARRY 40-80 SERRARE O'-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                            Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L., "The G glycoprotein of human respiratory syncytial viruses of subgroups A and B. extensive sequence divergence between
                                                                                                                                                          Human respiratory syncytial virus (subgroup A / strain Long).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.9%; Score 1216; DB 1; Length 298; 99.1%; Pred. No. 4.3e-75; Live 0; Mismatches 2; Indels (
                                                               01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI TaxID=11260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. EXTRACELLULAR (POTENTIAL)
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InterPro; IPR000925; Glycoprot G.
Pfam; PP00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=87289657; PubMed=2441388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32781 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.1
Matches 230; Conservative
                                   STANDARD:
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298
1103
1135
2237
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251
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135
135
237
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251
294
298 AA;
                                 VGLG HRSVL
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RESULT 1
VGLG_HRSVL
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us-09-462-816-4.rsp

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126
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                                                                       QPITVKTKNTITTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
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-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.

-!- SUBCELLILLAR LOCATION: EXPRESSED ON THE SURFACE OF THE INPECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRLONS.

-!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINB AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE=95566153; PubMed=7747420; Connors M., Crowe J.E. Jr., Firestone C.Y., Murphy B.R., Collins P.L.; "A cold-passaged, attenuated strain of human respiratory syncytial virus contains mutations in the F and L genes."; Virus Cott 478-484 (1995).
                             67 HKVTLTTAIIQDATSQIKNTTPTVLTQDPQLGISFSNLSEITSQTTILASTTPGVKSNL
                                                                                               QPTIVKTKNITITIOTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALC
                                                                                                                                             KR.I PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTBEPTINTTKTNITTT
HKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                           KRIPNKKPGKKTTTKPTKKPTFKTTKKDHKPQTTKPKEVPTTKPTEBPTINTKTNIITT
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(L)
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MEDLINE=85216636; PubMed=3858865;
Wertz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.;
"Nucleotide sequence of the G protein gene of human respiratory
syncytial virus reveals an unusual type of viral membrane protein.",
Proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).
                                                                                                                                                                                                                       181 LLTINNTIGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Acquistion of the ts phenotype by a chemically mutagenized cold-
passaged human respiratory syncytial virus vaccine candidate resul
from the acquisition of a single mutation in the polymerase (L)
                                                                                                                                                                                                                                               247 LLINNTIGNPKLISOMETPHSISSEGNLSPSQVSTISEHPSQPSSPPNTIRQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-86067198; PubMed-4069997;
Satake M., Coligan J.E., Elango N., Norrby E., Venkatesan S.;
"Respiratory syncytial virus envelope glycoprotein (G) has a r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97187925; PubMed=9035372;
Crowe J.E. Jr., Firestone C.Y., Whitehead S.S., Collins P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus (strain A2).
Viruses; sRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI TaxID=11259;
                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        298 AA.
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VGLG_HRSVA
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Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
Subgroup A respiratory syncytial viruses.";
J. Gen. Virol. 72:2091-2096(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE HEMAGGLUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURPACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRONS.
-!- FTM: MAX CARRY 40-80 SERRANG O-LINKED CARBOHYDRATE CHAINS
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HKVTPTTAIIQDATSQIKNTTPTYLTQNPQLGISPSNPSBITSQITTILASTTPGVKSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 OPTIVKIKNITITOTOPSKPITKORONKPPNKPNNDFHFEVFNFVPCSICSNNPICWAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 LLISNITGNPELISOMETFHSTSSEGNPSPSQVSTISEYPSQPSSPDNTPRQ 298
                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                           91.1%; Score 1120; DB 1; Length 298; 92.7%; Pred. No. 1.2e-68; ive 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  12; Indels
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                       67 296 EXTRACELLULAR (POTENTIAL).
135 135 N-LINKED (GLCNAC. .) (PO
237 237 N-LINKED (GLCNAC. .) (PC
251 251 N-LINKED (GLCNAC. .) (PC
254 251 851 N-LINKED (GLCNAC. .) (PC
258 AA; 32586 MW; 993C3D2DD68BC634 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein
                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human respiratory syncytial virus (strain rsb6256)
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                                                                                                                                                                                     InterPro, IPR000925; Glycoprot G. Pfam; PF00802; Glycoprotein G; 1. Transmembrane; Glycoprotein.
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InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; 1.
                                                                                 EMBL; M11486; AAB59857.1; --
EMBL; X03149; CAAZ6928.1; --
EMBL; US0362; AAB8665.1; --
EMBL; UG0363; AAB86675.1; --
EMBL; UG3644; AAC55969.1; --
PIR; A94048; MGNZ.
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 215; Conservative
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                                                                                                                                                                                                                                                            66
298
135
237
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P27025;
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TRANSMEM
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CARBOHYD
CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                     121 KRIPNKKPGKKTTTKPTKKPTFKTTKKOLKPQTTKPKEVPTTKPTBEPTINTTKTNITT 180
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Cane P.A., Matthews D.A., Pringle C.R.;

Cane P.A., Matthews D.A., Pringle C.R.;

Cane P.A., Matthews D.A., Pringle C.R.;

Cane P.A., Matthews D.A., Pringle C.R.;

Cane V. Matthews D.A., Pringle C.R.;

J. Gen. Virol. 72:2091-2096(1991).

-!- FUNCTION. UNLIKE THE OFFER PARAMYZOVIRUS ATTACHMENT PROTEINS, THE PERPIRATORY SYNCYTIAL PIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEWAGGIOTINATING ACTIVITIES.

-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

-!- PTW. MAY CARRY 40-80 SEBRARAE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                    0; Gaps
                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                    85.6%; Score 1052; DB 1; Length 297;
                                                                                                                                                                                                Pred. No. 4.2e-64;
6; Mismatches 23; Indels
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                     -LINKED (GLCNAC. . .) (PC
6781756C38B64A80 CRC64;
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                                              EXTRACELLULAR (POTENTIAL)
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                CYTOPLASMIC (POTENTIAL).
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Glycoprotein.
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nes 201; Conservative
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297 AA;
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Best Local Similarity
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P27022;
            DOMAIN
TRANSMEM
DOMAIN
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CARBOHYD
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Score 1045; DB 1; Length 297; Pred. No. 1.3e-63;

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                                                                                                      67 HKITSTTTIQDATNQIKNTTPTYLTQNPQLGISPSNPSDITSLITTLDSTTPGVKSTL 126
                                                                                                                                                                                                 61 OPTIVKIKNTITIQIQPSKPITKQRQNKPPNKPNNDFHFBVFNFVPCSICSNNPICWAIC 120
                                                                                                                                                                                                                                        127 QSTTVGTKNTTTTQAQPNKPTTKQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
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                                                                  1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
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J. Gen. Virol. 72:2091-2096(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLLA AND INCORPORATED IN THE MEMBRARD OF THE VIRIONS.
-!- PTM: MAY CARRY 40-80 SEPRARTS O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91374005; PubMed=1895054; Cane P.A., Matthews D.A., Pringle C.R.; Identification of variable domains of the attachment (G) protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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135 N-LINKED (GLCNAC. . .) (POTENTIAL).
237 N-LINKED (GLCNAC. . .) (POTENTIAL).
251 N-LINKED (GLCNAC. . .) (POTENTIAL).
294 N-LINKED (GLCNAC. . .) (POTENTIAL).
32670 MM; 58B384028E437ACD CRC64;
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Pred. No. 4.3e-63;
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   200; Conservative 10; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus (strain rsb6614).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
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67 HKVTLTTAIIQDATSQIKNTTQTYLTQNTQLGISFSNLSETTSQPTTTPALTTPSAKSTP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTEEPTINTTKTNITTT 180
                            187 KRIPNKKPGKKTTTKPTKKPTKTTKTDLKPQTTKPKEVLTTKPTEKPTINTTKTNIRTT 246
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0; Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                181 LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                               247 LLTINITGNPEYISQKETLHSTSPEGNPSPSQVYITSEYPSQPPSPSNIT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLTNNTTGNPKLTSQMBTPHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT
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Pred. No. 8e-63; lndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human respiratory syncytial virus (strain rsb5857).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last amnotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 N-LINKED (GLCNAC. . .) (PC
32772 MW; 10488CCA475936BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                          PRT;
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86.5%;
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                                                                                                                                                                                                                                                                        STANDARD;
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103
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                                                                                                                                                                                                                                                                        VGLG HRSV4
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VGLG HRSV4

ID VGLG HRSV4

ID DT 01-AUG

DT 01-AUG

DE Major 01-AUG

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VGLG HRSV5 RESULT 7

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61 OPTTVKTKUTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFBVFNFVPCSICSNNPTCWAIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE=91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";
J. Gen. Virol. 72:2091-2096(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 EXTRACELLULAR (POTENTIAL).
103 N-LINKED (GLCNAC. . ) (POTENTIAL).
135 N-LINKED (GLCNAC. . ) (POTENTIAL).
237 N-LINKED (GLCNAC. . ) (POTENTIAL).
250 N-LINKED (GLCNAC. . ) (POTENTIAL).
294 N-LINKED (GLCNAC. . ) (POTENTIAL).
32769 MM; 4D74E85413407BBS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- FTW. MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
PIR, JQ1207; JQ1207.
InterPro; IPRO00925; Glycoprot, G.
Pfam; PF00802; Glycoprotein.
Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
тея 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human respiratory syncytial virus (strain rsb642).
Viruses; ssRNA negative strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI TaxID=11225;
                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last amnotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                      Human respiratory syncytial virus (strain rsb6190).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11255;
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298 AA.
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tive 10; Mismatches
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PRT;
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Matches 197; Conservative
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STANDARD;
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VGLG HRSV5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HKVTLTTAIIQDATSQIKNTTFTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
                                                                                                         subgroup A respiratory syncytial viruess.", J. Gen. Virol. 72:2091-2096(1991).

-!- FUNCTION: VALIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                         MEDLINE=91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment (G) protein of
                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
PIR; JQ1204; JQ1204.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.1%; Score 1009; DB 1; Length 297;
84.0%; Pred. No. 3.2e-61;
ive 11; Mismatches 26; Indels 0
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01-NOV-1991 (Rel. 20, Last sequence update)
01-MUG-1992 (Rel. 23, Last amnotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
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Sullender W.M., Mufson M.M., Anderson L.J., Wertz G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
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67 297 EX
135 135 N-
144 N-
237 237 237 N-
297 AA; 32745 MW;
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Virology 178:195-203(1990).
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                        SEQUENCE FROM N.A.
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TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 KRIPNKKPGKKTTTKPTKKPTFKTT-KKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 179
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                    respiratory syncytial viruses...,
J. Virol. 65:5425-534 (1991).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
HEMAGGLUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURRACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANB OF THE VIRIONS.
-!- PTM: MAY CARRY 40-80 SEPRARYE 0-LINKED CARBOHYDBATE CHAINS
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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Viruses; seRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-87289557; PubMed-2441388;
Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
"The G glycoprotein of human respiratory syncytial viruses of
subgroups A and B: extensive sequence divergence between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.1%; Score 505.5; DB 1; Length 292;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-RVOV-1991 (Rel. 20, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
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"Genetic diversity of the attachment protein of subgroup
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EXTRACELLULAR (POTENTIAL)
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BEC60C85EF057BB5 CRC64;
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67 292 EX
81 81 N-
86 86 N-
100 100 N-
292 AA; 32143 MW;
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EMBL; M73545; AAA47408.1; -.
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tes 108; Conserv
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VGLG_HRSV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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EMBL; X01918; CAA25994.1; -.
EMBL; AE003544; AAF50056.1; -
EMBL; X78392; CAA55154.1; -.
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HKVTLTTVTVQTIKNHTEKNISTYLTQVPPERVNSSKQPTTTSPIHTNSATISPNTKSET 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 OPTIVKTKNITITIQIQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRIPNKKPGKKTTTKPTKKPTPKTT-KKDLKPQTTKPKEVPTTKPTBEPTINTTKTNITT 179
          Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-83294545; PubMed-6411930;
Garfinkel M.D., Pruitt R.E., Meyerowitz E.M.;
"DNA sequences, gene regulation and modular protein evolution in the
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                        -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopiera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                       40.4%; Score 497; DB 1; Length 292; 46.8%; Pred. No. 6.9e-27; rative 28; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 TLLINNTIGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPS 221
                                                                                                                                                                                                                                                                                                66 POTENTIAL.
292 EXTRACELLULAR (POTENTIAL).
81 N-LINKED (GLCNAC. .) (PO
86 N-LINKED (GLCNAC. .) (PO
100 N-LINKED (GLCNAC. .) (PO
32306 MW; BC8C59F69CA7AFCZ CRC64;
                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 SQSTVLDTITPKYTIQQQSLHSTTSENTPSSTQIPTASE-PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P02840; O9VTU2;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Salivary glue protein Sgs-3 precursor.
SGS3 OR CG11720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 AA
                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila 68C glue gene cluster.";
J. Mol. Biol. 168:765-789(1983).
                                                                                                                                                                                                                                   PIR, B32703; MGNZ18.
InterPro.; IPRODOS25; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; Iransmembrane; Glycoprotein.
antigenically related proteins.";
                                               HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                                        EMBL; M17213; AAA47412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                              292 AA;
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                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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93; Indels 48; Gaps 13;
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                                                                                                                                                                                                                                                                    137 QLPCTTPTTTKPTTTKPTTTKPT--TTKPTTTKPTTTKP---TTTTKPT-1TTKPT--TTKPT 189
                                                                                                                                                                                        62 PTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICK 121
                                                                                                                                        4 TLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGV--KSNLQ 61
                                                                                                                                                                49 TTTTTTCAPPTQQ-STTQPPCTTSKP-----TTPKQTTTQLPCTTPTTKATTTK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE FROM N.A.
MEDLINE=99018118; PubMed=979973;
Glocknes G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
Glocknes G., Rosenthal A.;
"Large-scale sequencing of two regions in human chromosome 7q22:
analysis of 650 kb of genomic sequence around the BPO and CUTL1 loci
reveals 17 genes.";
Genome Res. 8:1060-1073 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miller W., Koop B.F., "Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5."; Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                                                                                                              177 ITTILITNNTIGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTR 231
                                                                                                                                                                                                                                                                                                            190 TTKPTTTKPTTTKPTTTKPTTTKPTTTKPTTTKPT--TTKPTTTK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gao Z., Harumi T., Garbers D.L.; "Chromosome localization of the mouse zonadhesin gene and the human zonadhesin gene (ZAN).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21138439; PubMed=11239002;
Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                 ZAN_HUMAN STANDARD, PRT; 2812 AA.
Q9Y493; Q00218; Q96L85; Q96L87; Q96L88; Q96L90;
Q9BXN9; Q9BZ83; Q9BZ84; Q9BZ86; Q9BZ86; Q9BZ87; Q9BZ88;
                                                                                   / Match 16.4%; Score 202; DB 1; Length 307; Local Similarity 32.8%; Pred. No. 4.4e-07; les 77; Conservative 17; Mismatches 93; Indels 4
                                   1 23 POTENTIAL.
24 307 SALIVARY GLUE PROTEIN SGS-3.
307 AA, 32196 MW, 45803DED16C418BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE Testis;
Cheung T.L., Wassler M.J., Cornwall G.A., Hardy D.M.;
"Multiple intra-species variants of human zonadhesin.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).
                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 2375-2683 FROM N.A. (ISOFORM 7).
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            FlyBase; FBgn0003373; Sgs3.
Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zonadhesin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
PIR; A03329; GSFF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=9606;
                                                            SEQUENCE
                                                                                     Query Match
                                    SIGNAL
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Genomics 41:119-122(1997).
-!- FUNCTION: BIRDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA OF THE BGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR SIGNALING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- DOWAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRAPTING OF THE WIGUN-LIKE DOWAIN MIGHT INHIBIT INAPPROPRIATE TRAPTING OF SPERMANOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
-I- DOWAIN: The VWFD domain 2 may mediate covalent oligomerization (by similarity to human intestinal mucin MUC2).
-I- SIMILARITY: Contains 3 MAM domains.
-I- SIMILARITY: Contains 4 VWFD domains.
-I- SIMILARITY: Contains 1 RGF-like dowain.
-I- SIMILARITY: Contains 1 RGF-like dowain.
-I- SIMILARITY: Contains 1 RGF-like dowain.
-I- SIMILARITY: Contains 1 RGF-like dowain.
-I- SIMILARITY: Contains 1 RGF-like dowain.
-I- SIMILARITY: Contains 1 RGF-like dowain.
                                                                                                                                                              -!- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOId=Q9Y493-7; Sequence=VSP_001426, VSP_001427; --: TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.-:- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLICIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO: GO:0016324; C:apical plasma membrane; NAS.
GO: GO:000733; P:blading of sperm to zona pellucida; NAS.
GO: GO:0008037; P:cell recognition; NAS.
GO: GO:0016337; P:cell-cell adhesion; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=1;
IsoId=Q9Y493-2; Seguence=VSP_001430, VSP_001431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9Y493-4; Sequence=VSP_001424, VSP_001425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9Y493-5; Sequence=VSP_001420, VSP_001421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9Y493-6; Sequence=VSP_001422, VSP_001423;
                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9Y493-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMEL, AY046055; AAL04411.1; ...
EMEL, AY046055; AAL04412.1; ...
EMEL, AY046055; AAL04413.1; ...
EMEL, AY046055; AAL04414.1; ...
EMEL, AY046055; AAL04414.1; ...
EMEL, AY046055; AAL04415.1; ...
EMEL, AY01303; AAX10411.1; ...
EMEL, U83191; AAX21011.1; ...
GENEW, HGNC:12857; ZAN.
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InterPro; IPR000999; MAM domain.
InterPro; IPR0032919; TLL Cysrich.
InterPro; IPR001328; TLLa Cysrich.
InterPro; IPR001007; VWF G.
InterPro; IPR001007; VWF G.
Prestro; IPR0014846; VWF D.
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EMBL, AF332977; AAK01432.1; --
EMBL, AF332977; AAK01433.1; --
EMBL, AF332977; AAK01434.1; --
EMBL, AF332978; AAK01435.1; --
EMBL, AF332980; AAK01435.1; --
EMBL, ARV406055; AAL04410.1; --
EMBL, AY046055; AAL04411.1; --
EMBL, AX046055; AAL04412.1; --
EMBL, AX046055; AAL04412.1; --
EMBL, AX046055; AAL04412.1; --
EMBL, AX046055; AAL04412.1; --
EMBL, AX046055; AAL04413.1; --
                                                                                                                                                                                                                                                                                             -! - ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                 Name=3;
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MUC2_HUMAN
ID _MUC2_HUMAN
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DR Pfam; PF02345; TILL; 4.

DR Pfam; PF002945; TILLa; 5.

DR SWART; SW00181; EGF; 4.

DR SWART; SW00181; EGF; 4.

DR SWART; SW00215; VWC_out; 4.

DR SWART; SW00215; VWC_out; 4.

DR SWART; SW00215; VWC_out; 4.

DR SWART; SW00216; VWD; 4.

DR PROSITE; PS00740; MAM_1; 1.

DR PROSITE; PS00740; MAM_1; 1.

DR PROSITE; PS00740; MAM_1; 1.

DR PROSITE; PS00740; MAM_1; 1.

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RLCLQWHPEPPLADCGCTSNGIYYQLGSSFLTEDCSQRCTC
ASSRILLCEPP -> YAILCQBAGAALAGWRDRTLCAMBCP
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PASCANLADPGDCEGPCVEGCAD (in isoform 7).
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AGQQ (in isoform 7).
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
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                                                   DGQCR -> YAILCQBAGAALAGWRRRTLCAMBCDAGTIYO
SCWTPCPASCANLADPGDCEGPCVEGCASIPGYASGTQSL
PWLTYVAAPAWASTTRSELAAGGPGEQRRQGEPDQGWNWNVS
SWPFPPLAGQQLSD (in 180form 1).
 HGVSSRYHISELYDTLPSILCQPGRPRGLRGPLRGRLRQHP
                    RLCLQWHPEPPLADCGCTSNGIYYQLGSSFLTEDCSQRCTC
                                      ASSRILLCEPFSCRAGEVCTLGNHTQGCFPESPCLQNPCQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 TINITKTNITT-----TLLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVST----
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                                                                                                                                                                                                                                                                                                                                                                                          "The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstream and downstream of its central repetitive region."; [3]
                                                                                                                                                                                                                                                           Gaps
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"Molecular cloning of human intestinal mucin (MUC2) cDNA.
Identification of the amino terminus and overall sequence similarity
to prepro-von Willebrand factor.";
J. Biol. Chem. 269:2440-2446(1994).
[2]
SEQUENCE OF 626-1895 AND 4196-5179 FROM N.A.
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MEDLINES-13158717, PubMed=1885763;
TOTIDARA N.W., Gum J.R., Jr., Culhane P.J., Lagace R.E., Hicks J.W.,
Petersen G.M., Kim Y.S.;
                                                                                                                                                                                 H -> Q (IN REF. 1; AAK01431/AAK01432/
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Colon;
MEDILINE=93016075; PubMed=1400449;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe E.-M., Lagace R.E.
Kim Y.S.;
                                                                                                                                                                                                                     ; Score 198.5; DB 1; Length 2812; Pred. No. 7.4e-06; 35; Mismatches 91; Indels 59;
                                                                                                                           /FTId=VSP_001430.
Missing (in isoform 1).
/FTId=VSP_001431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                002817; 014878;
01-JUN-1994 (Rel. 29, Created)
01-NV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
MUCIN 2 precursor (Intestinal mucin 2).
HOMO sapiens (Human).
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SEQUENCE FROM N.A.
TISSUB=Intestine;
MEDLINE=9413200571;
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      and polymorphism.";
and polymorphism.";
d. Ciln. Invest. 88:1005-1013(1991).
d. Ciln. Invest. 88:1005-1013(1991).
c. FUNCTION: COATE THE BETTHELIA OF THE INTESTINES, AIRWAYS, AND OTHER WICHS MEMBRARAS-CONTAINING ORGANS. THOUGHT TO PROVIDE A PROTECTIVE, IUBRICATING BARRIER AGAINST PARTICLES AND INFECTIOUS AGBNESS AT MUCUSAL SURFACES.
c. 1- SUBCELLULAR LOCATION: Secreted.
c. 1- SUBCELLULAR LOCATION: Secreted.
c. 1- SUBCELLULAR LOCATION: Secreted.
c. 1- SUBCELLULAR LOCATION SMALL INTESTINE, COLONIC TUMORS, BRONCHUS, CERVIX AND GALL BLADDER.
c. 1- SUBCELLULAR ESIDIES ARE INVOLVED IN INTRACHAIN OR BRONCHUS, CERVIX AND GALL BLADDER.
c. 1- SUBCHIALD SMADNE DIFFERENT ALLELES.
c. 1- POLYMORPHISM: THE WUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND VARIES AMONG DIFFERENT ALLELES.
c. 1- SIMILARITY: Contains 1 C-terminal cystine knot-like) domain.
c. 1- SIMILARITY: Contains 2 VWFC domains.
"MUC-2 human small intestinal mucin gene structure. Repeated arrays
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EMBL; M74027; AAA59875.1; -.
EMBL; M94131; AAA59163.1; -.
EMBL; M94132; AAA59164.1; -.
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Best Local Similarity 30.6%; Pred. No. 3.3e-05;
Matches 77; Conservative 23; Mismatches 114; Indels 38; Gaps
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                                                                                                                                               MEDLINE=93077556; PubMed=1447205;
A Hauser F., Hoffmann W.;
T. "P-domains as shuffled cysteine-rich modules in integumentary mucin T. T. (FIM-C.) from Xenopus laevis. Polydispersity and genetic polymorphism.";
J. Biol. Chem. 267:24620-24624(1992).
L. Grine. Could be involved in defense against microbial infections. Protects the epithelia from external environment.
C. I. SUBCELLULAR LOCATION: Secreted.
C. I. ALTERNATIVE RRODOUTS:
C. Comment=Alternative splicing; Named isoforms=7;
Comment=Additional isoforms seem to exist. Experimental
C. Comment=Additional and be lacking for some isoforms;
                                                                                                                                                                                                                                                                                                                                                      IsoId=005049-5; Sequence=VSP_004646, VSP_004649, VSP_004650;
                                       01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
28-FRB-2003 (Rel. 41, Last annotation update)
Integumentary mucin C.1 (FTM-C.1) (Fragment).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopus latrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                     IsoId=Q05049-4; Sequence=VSP_004647, VSP_004648;
                                                                                                                                                                                                                                                                                                                                                                        Isold=205049-6; Sequence=VSP_004646, VSP_004648;
                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6 AND 7)
TISSUE=Skin;
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INTERPRO, IPRO00519; Prefoil.
Pfam; PR00088; trefoil.
FRINTS; PR00680; PRREFOIL.
SMART; SM0018; PD; 6.
PROSITE; PS00025; PTREFOIL, 6.
Repeat, Glycoprotein; Alternative splicing.
NOW TER 1 144 8 X 8 AA APPROXIM
                        662 AA.
                                                                                                                                                                                                                                                                                                IsoId=Q05049-2; Sequence=VSP_004650;
                                                                                                                                                                                                                                                                                                                   IsoId=205049-3; Sequence=VSP_004651;
                                                                                                                                                                                                                                                                                                                                                                                          ISOId=005049-7; Sequence=VSP_004647;
-!- TISSUE SPECIFICITY: SKIN.
-!- PTM: EXTENSIVELY O-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                 IsoId=Q05049-1; Sequence=Displayed;
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                        STANDARD;
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                                                                     288 TPÍTITÍKAÍTÍTÍTÍTSGECKMEPSKREDCGYSGIÍTESÓCRTKGCCFDSSIÞQTKWCFYT 347
                                                                                                              93 -- PNNDFHFEVFNFVPCSI-----CSNNPTC------WAICKRIPNKKPGKKTTT 134
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14.9%; Score 183; DB 1; Length 217;
Best Local Similarity 33.3%; Pred. No. 5.8e-06;
Matches 55; Conservative 10; Mismatches 68; Indels 32; Gaps
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MEDLINE=88332966; PubMed=3138416;
Martin C.H., Mayeda C.A., Mayerowitz E.M.;
"Evolution and expression of the Sgs-3 glue gene of Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGS3.

Drosophila simulans (Fruit fly).

Drosophila simulans (Fruit fly).

Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,

Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha;

Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7240;
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24 217 SALIVARY GLUE PROTEIN SGS-3.
217 AA; 22750 MW; D29894E340257881 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Mol. Biol. 201:273-287(1988).
-!- DEVELOPMENTAL STACE: PRODUCED BY THIRD-INSTAR LARVAE.
PIR; S01358; 801358.
FlyBase; FBGn0012853; Dsim\Sgs3.
                                                                                                                                                                                                                                                                      195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPRNTT 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1990 (Rel. 13, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Salivary glue protein 8gs-3 precursor.
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OM protein - protein search, using sw model

Run on:

October 29, 2003, 17:33:35; Search time 22.3245 Seconds (without alignments) 999.400 Million cell updates/sec

Perfect

US-09-462-816-4 1229 1 HKVTLTTAIIQDATSQIKNT.....VSTTSEHPSQPSSPPNTTRQ 232 score:

BLOSUM62 Gapop 10.0 , Gapext Scoring table: Sequence:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB a

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		* Query			SUMMARIES	
No.	Score	Match	Length	8	QI	Description
Н	1216	98.9		н	MGNZRL	major surface glvc
01	1120	91.1		~	MGNZ	
٣	1052	85.6	297	N	JQ1208	attachment protein
4	1045	85.0		7	JQ1205	
Ŋ	1042	84.8		~	JC5680	•
9	1037	84.4		~	JQ1209	ل ت
7	1033	84.1		N	JQ1206	
œ	1019	82.9		N	JQ1207	
a	1009	82.1		~	JQ1204	
10	505.5	41.1		Н	MGNZ60	æ
11	497	40.4		Ч	MGNZ18	major surface glvc
7	425	34.6		ч	ZNHA	nucleocapsid prote
<u>~</u>	202	16.4		Н	GSFF3	salivary olue prot
4	193	15.7		N	A43932	mucin 2 precursor.
π	191	15.5	662	N	A45155	mucin FIM-C.1 - Af
9	190	15.5		N	A53715	abomucin precursor
_	188	15.3		~	T31113	mucin-like glycopr
8	186.5	15.2		~	T22696	hypothetical prote
9	185.5	15.1	379	8	S50125	larval glue protei
0	183	14.9		N	S01358	Balivary glue prot
덙	183	14.9	-	N	S57180	probable membrane
22	179	14.6		~	T46740	microfilarial ghea
33	178	14.5	250	N	PQ0768	·
4.	177			н	MGNZBR	7
S.	175	14.2		N	T22808	
9	175	14.2		~	T29634	
-	172.5	14.0	327	~	S20074	
œ :	171.5	14.0	216	N	151920	9
53	170.5	13.9	263	N	JQ2284	glycoprotein G - b

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S53363	T34022	A37232	E86185	820075	853362	862335	801360	J02388	T34369	A53577	PO0769	A48732	A48292	T34513
7 7	N	N	0	N	N	7	N	0	7	N	8	C	l C	(7)
1367	2476	294	402	371	477	393	263	263	1777	1630	248	263	1118	3507
13.9	4.	3.3	3.3	3.3	3.3	3.1	3.0	3.0	6.2	8.2	8.2	7.7	9.8	5.5
HH	H	H	H	H	H	H	H	H	H	ä	H	1	1	7
170.5	164.5	163.5	163.5	163	163	160.5	160	159.5	158	157.5	157	156.5	155	153.5
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ALIGNMENTS

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major surface glycoprotein G - human respiratory syncytial virus (strain Long)
C,Species: human respiratory syncytial virus
C,Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C,Accession: A32703; S12279
E,Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and A;Reference number: A32703; MUID:87289657; PMID:2441388

A; Accession: A32703
A; Molecule type: mRNA
A; Residues: 1-298 < JOH>
A; Molecule type: mRNA
A; Residues: 1-298 < JOH>
A; Cross-references: GB:M17212; NID:g333940; PIDN:AAA47411.1; PID:g333941
A; Garcia-Barreno. B.; Portela, A.; Delgado, T.; Lopez, J.A.; Melero, J.A.
BRBO J. 9, 4181-4187, 1990
A; Hille: Frame shift mutations as a novel mechanism for the generation of neutralizat: A; Reference number: S12279; MUID:91065351; PMID:2249671
A; Reference number: S12279
A; Molecule type: mRNA
A; Residues: 1-298 < GAR>
C; Mesidues: 1-298 < GAR>
C; Mesidues: 1-298 < GAR>
C; Mesidues: 1-298 < GAR>
C; Meywords: glycoprotein; transmembrane protein
F; 41-63/Domain: transmembrane #status predicted < TWN>
F; 85, 103, 135, 179, 237, 250, 251, 273, 294/Binding site: carbohydrate (Asm) (covalent) #stal

Query Match

98.9%; Score 1216; DB 1; Length 298;
Best Local Similarity 99.1%; Pred. No. 5.8e-75;
Matches 230; Conservative 0; Mismatches 2; Indels

ô 67 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 126 9 1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSRITSQTTTILASTTPGVKSNL Gaps ö ઠ 뭐

61 OPTIVKIKNITITOTOPSKPITKORONKPPNKPNNDFHFBVFNFVPCSICSNNPTCWAIC 120 ò 셤

KRIPNKKPGKKTTTKPTKKPTFKTTKKOLKPQTTKPKEVPTTKPTBEPTINTTKTTT 180 121 Š 셤

246

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RESULT 2

MGNZ major surface glycoprotein G - human respiratory syncytial virus C;Species: human respiratory syncytial virus C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 24-Sep-1999

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C;Species: Human respiratory syncytial virus
C;Date: 11-Nov-1997 #sequence_revision 11-Nov-1997 #text_change 26-Feb-1998
C;Accession: JC5680
C;Accession: JC5680
X; Wang, Z; Qian, Y; Zhu, R; Deng, J; Du, J; Zhu, Z.
Chinese J. Virol. 12, 317-322, 1996
A;Title: Molecular analysis of G protein gene of a respiratory syncytial virus strain is: A;Reference number: JC5680
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A;Note: the authors translated the codon TTT for residue 165 and 170 as Glu, TTC for res
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
F;1-38/Domain: intracellular #status predicted <INT>
F;39-66/Domain: transmembrane #status predicted <ITM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il ildren and adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                attachment protein - human respiratory syncytial virus (strain RSB1734)
NyAlternate names: G protein
C;Species: human respiratory syncytial virus
C;Species: human respiratory syncytial virus
C;Accession: J01205
R;Cane, P.A.; Matthews; D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A, A,Reference number: J01204; MUID:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 KRIPNKKAPGKRITIKPTKKTPKTITKKGPKPQTIKSKEAPITKPTEEPIINITITI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
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                                                                                                 127 QSTTVKTKNTTTTQIQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
                                                                                                                                                                                                                                121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTBEPTINTTKTNITTT 180
                                                                                                                                                                                                                                                                                   187 KRIPNKKPGKKTTTKPTKKPIKTTKKDLKPQTTKPKEVLTTKPTEKPTINTTRTNIRTT 246
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                              61 QPTTVKTKNTTTTQTQBSKPTTKQRQNKPPNKPNNDFHFEVFBVFCSICSNNPTCWALC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                        181 LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 LITTNTTGNPEYTSQXETLHSTSPEGNPSPSQVYTTSEYPSQPPSPSNTT 296
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A; Residues: 1-297 < CAN>
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A; Residues: 1-298 <GEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid protein A.Note: this protein may carry 40-80 separate O-linked carbohydrate chains distributed a R.Satake, M.; Coligan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S. Nucleic Acids Res. 13, 7795-7812, 1985 A.Fitle: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure. A.Reference number: A93599; MUID:86067198; PMID:4069997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attachment protein - human respiratory syncytial virus (strain RSB6256)
N.A. Learnate names: G protein
C.Species: human respiratory syncytial virus
C.Species: human respiratory syncytial virus
C.Species: al.Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C.Accession: 071208
R.Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A.Title: Identification of variable domains of the attachment (G) protein of subgroup A A, Reference number: 071204, MuID:91374005, PMID:1895054
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C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217; GH
                              Riwertz, G.W.; Collins, P.L.; Huang, Y.; Gruber, C.; Levine, S.; Ball, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985
A;Title: Nucleotide sequence of the G protein gene of human respiratory syncytial virus
A;Reference number: A94048; MUID:85216636; PMID:3858865
A;Accession: A94048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:X03149; NID:g60997; PIDN:CAA26928.1; PID:g60998
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 LLITNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.1%; Score 1120; DB 1; Length 298; 92.7%; Pred. No. 1.6e-68; tive 5; Mismatches 12; Indels (
C; Accession: A94048; A93599; A04039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 92.78
Matches 215; Conservative
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Best Local Similarity
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A,Residues: 1-297 <CAN>
C,Comment: Respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-298 <SAT>
                                                                                                                                                                                                                                                                                                                            A; Residues: 1-298 <WER>
                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
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Ajaccession: JQ1207
Ajmolecule type: mRNA
AjResidues: 1-298 «CANA
Ajresidues: 1-298 «CANA
Ajresidues: 1-298 «CANA
Ajresidues: 1-298 «CANA
Ajresidues: 208 «CANA
Ajresidues: 208 «CANA
Ajresidues: 208 «CANA
Ajresidues: 1-298 «CANA
Ajresidues: 1-298 «CANA
Ajresidues: 1-298 «CANA
CANA
CICOMMENT: Respiratory syncytial virus major surface glycoprotein G
Circywords: 3lycoprotein; transmembrane protein
F;85,103,135,237,250,273,294/Binding site: carbohydrate (Asn) (covalent) #status pred
                                                              Afacession: JQ1206
A;Molecule type: mRNA
A;Residues: 1-27 <CAN>
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
ildren and adults.
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Reywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attachment protein - human respiratory syncytial virus (strain RSB6190)
NyAlternate names: G protein
C;Species: human respiratory syncytial virus
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1207
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
A;Tene, P.A.; Matthews, D.A.; Pringle, C.R.
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A;Reference number: JQ1204; MUID:91374005; PMID:1895054
A,Title: Identification of variable domains of the attachment (G) protein of subgroup A,Reference number: JQ1204, MUID:91374005, PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVPNFVPCSICSNNPTCWAIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                    84.1%; Score 1033; DB 2; Length 297; 86.5%; Pred. No. 1.2e-62; tive 5; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.9%; Score 1019; DB 2; Length 298; Best Local Similarity 84.9%; Pred. No. 1e-61; Matches 197; Conservative 10; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 199; Conservative
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Best Local Similarity
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NyAlternate names: G protein

NyAlternate names: G protein

C;Species: human respiratory syncytial virus

C;Dete: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Reb-1997

C;Accession: JO1209

R;Cane, P.A.; Matthews; D.A.; Pringle, C.R.

J; Gen. Virol. 72, 2091-2096, 1991

A;Title: Identification of variable domains of the attachment (G) protein of subgroup A A;Title: Identification of variable pringle, PMID:1895054

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Residues: 1-297 c.CAN>

C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract iller children, and adults.
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C;Reywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
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                                                                                                                                                                                                                                                                                                                                                                                                            127 QSTTVKTKONTTTTQIQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCMAIC 186
                                                                                                                                                                                                                                                                                                                                                                            QPITVKTKNTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KRIPNKKPGKKTTTKPTKKPTFKTTKKOLKPQTTKPKEVPTTKPTBEPTINTTKTNITT 180
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N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: UQ1206
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
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                                                                         Query Match

84.8%; Score 1042; DB 2; Length 298;
Best Local Similarity 86.6%; Pred. No. 2.9e-63;
Matches 201; Conservative 8; Mismatches 23; Indels (
           F;67-298/Domain: extracellular #status predicted <BXC>
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major surface glycoprotein G - human respiratory syncytial virus (strain 18537)
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: B32703
R;Johnson, P.R; Spriggs, M.K.; Olmeted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and lA;Reference number: A32703; MUID:87289657; PMID:2441388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRIPNKKPGKKTTTKPTKKPTFKTT-KKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 179
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Cipate: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
Cipatession: A04026
Rislango, N.; Venkatesan, S.
Nucleic Acids Res. 11, 5941-5951, 1983
A;Title: Amino acid sequence of respiratory syncytial virus capsid protein.
A;Reference number: A04026; MUID:83299261; PMID:6310521
A;Accession: A04026
A;Molecule type: mRNA
A;Residues: 1-467 < ELAb.
A;Cross-references: GB:X00001; NID:g61215; PIDN:CAA24906.1; PID:g61216
                                 127 HHTTAQTKGRITTSTQTNKPSTKSRSKNPPKKPKDDYHFEVFNFVPCSICGNNQLCKSIC
QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC
                                                                                                                                                           187 KTIPSNKPKKKPTIKPTNKPTTKTTNKRDPKTPAKMPKKEIITNPTKKPTLKTTERDTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 HKVTLITVIVQTIKNHTEKNISTYLTQVPPERVNSSKQPTTISPIHTNSATISPNTKSET
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A; Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
A; Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
A; Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
A; Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
A; Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
A; Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
A; Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: respiratory syncytial virus major surface glycoprotein C;Keywords: glycoprotein, transmembrane protein Tryl P;41-63/Domain: transmembrane #status predicted Tryl F;41-63/Domain: transmembrane #status predicted Tryl F;81,86,100/Binding site: carbohydrate (Asn) (covalent) #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleocapsid protein (version 2) - human respiratory syncytial virus
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                                                                                                                                                                                                                                                                   247 SQSTVIDITIPKYTIQQQSLHSTTSENTPSSTQIPTASE-PS-TSNP
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40.4%; Score 497; DB 1;
Best Local Similarity 46.8%; Pred. No. 1.3e-26;
Matches 104; Conservative 28; Mismatches 88;
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C;Superfam
C;Keywords
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MyAlternate names: attachment glycoprotein G
Species: human respiratory syncytial virus
C;Becies: human respiratory syncytial virus
C;Bote: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: A37077
S;Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A;Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis of a strict of the respiratory syncytial virus subgroup by the chance number: A37077; MUID:90357765; PMID:1697126
A;Reference number: A37077; MUID:90357765; PMID:1697126
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-292 <SUL>
A;Cosserreferences: EMBL:MS5633; NID:g333944; PIDN:AAA47413.1; PID:g333945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,144,237,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                            protein of subgroup
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                                                                                                       NiAlternate names: G protein
C;Species: human respiratory syncytial virus
C;Accession: J01204
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol, 72, 2091-2096, 1991
A;Fitle: Identification of variable domains of the attachment (G) protein of A;Reference number: J01204; MUD:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 KRIPNKKPGKRITITKPIKKPTLKTITKOPKPQTIKSEBVPITKLTEEPIINTITTITT
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                                                                               attachment protein - human respiratory syncytial virus (strain RSB642)
N;Alternate names: G protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.1%; Score 1009; DB 2; 84.0%; Pred. No. 4.8e-61; ive 11; Mismatches 26;
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47.6%; Pred. No. 3.5e-27;
tive 28; Mismatches 88
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Best Local Similarity 84.0%;
Matches 194; Conservative 1
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Best Local Similarity 47.6
Matches 108; Conservative
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A;Molecule type: mRNA
A;Residues: 1-297 <CAN>
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A; Gene: G
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A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 2037-3020
A; Residues: 2037-3020
A; Residues: 2037-3020
A; Residues: 2037-3020
A; Residues: 2037-3020
A; Residues: Sequence extracted from NCBI backbone (NCBIP:116698)
A; Note: sequence extracted from NCBI backbone (NCBIP:116698)
B; Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, C. Clin. Invest. 88, 1005-1013, 1991
A; Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polym. A; Reference number: A43932; MUID:913S8717; PMID:1885763
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A;Molecule type: mRNA
A;Readues: '', 1925-1948, 'TTS', 1952-1954 <JANN
A;Readues: '', 1925-1948, 'TTS', 1952-1954 <JANN
A;Readues: '', 1925-1948, 'TTS', 1952-1954 <JANN
B;Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstnation Biochem Biophys Rese Commun. 183, 821-828, 1992
A;Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the (A;Reference number: PQ0328; MUID:92198477; PMID:1550588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA A; Residues: 1343-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>
A; Residues: 1343-1350, 'L', 1352-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>
A; Crossreferences: GB:M74027; NID:g18863; FIDM:AAB59875.1; PID:g18864
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
B; Gun, 'J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6487, 1989
A; Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and evical control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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A;Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located both up A;Reference number: A45106; MUID:93016075; PMID:1400449
A;Accession: A45106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA Agreaduces: 1916-2193 (GU4> A;Residuces: 1916-2193 (GU4> A;Residuces: 1916-2193 (GU4> A;Cross-references: GB:M22405; NID:g188873; PIDN:AA36334.1; PID:g188874 A;Experimental source: intestine A;Experimental source: intestine Gum, J.R.; Kim, Y.S.; Basbaum, C.B. Glin. Invest. 87, 77-82, 1991 A;Elle: Human bronchus and intestine express the same mucin gene.
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A,Realdudes: 652-1895 - GUIZ>
A,Realdudes: 626-1895 - GUIZ>
A,Cross-references: GB:H94131; NID:g186395; PIDN:AAA59163.1; PID:g186396
A,Note: sequence extracted from NCBI backbone (NCBIP:116706)
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                                                                                                                                  A;Status: not compared with conceptual translation
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A;Residues: 2328-2342,'K',2344-2354 <XUG1>
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A; Residues: 2328-2468 < XUG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salivary glue protein ags-3 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 16-Jul-1999
C;Accession: A03229
R;Garfinkel, M.D.; Pruitt, R.E.; Meyerowitz, E.M.
A; Mal Biol. 168, 765-799, 1983
A;Title: Dh. sequences. gene regulation and modular protein evolution in the Drosophila A;Reference number: A92904; MUID:83294545; PMID:6411930
A;Reference number: Dh. A;Accession: A03329
A;Molecule type: Dh. A;Accession: A03329
A;Gorose-references: GB:X01918; NID:g8581; PIDN:CAA25994.1; PID:g603989
C;Goment: This protein is produced by third-instar larvae.
A;Gene: sgs-3
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NyAlternate names: mucin SMUC-41
NyAlternate names: mucin SMUC-41
Syspecies: Home sapiens (man)
C;Date: 10-Mar-1993 #sequence revision 12-Apr-1996 #text change 05-Nov-1999
C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329
R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.
A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the A;Reference number: A49963; MUID:94132002; PMID:8300571
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A Mesidues: 1-639 scdlr.
A Cross-references: GB1.21998
R Gum Jr., Jr., Hicks, J.W.; Toribara, N.W.; Rothe, E.M.; Lagace, R.E.; Kim, Y.S.
J. Biol. Chem. 267, 21375-21383, 1992
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                                                                                                                                            141 TFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTTLLTNNTTGNPKLTSQMETFH 200
                                                                                                                                                                                             376 TLKTTKKDPKPQTTKSKEVPTTKPTEEPTINTTKTNIITTLLTSNTTGNPELTSQMBTFH 435
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                                                          0; Gaps
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    90.2%; Pred. No. 1.5e-21;
tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                201 STSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
                                                                                                                                                                                                                                                                                                                                                                                436 STSSEGNPSPSQVSTTSEYPSQPSSPPNTPRQ 467
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C;Superfamily: salivary glue protein
C;Keywords: salivary gland; tandem repeat
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A;Map position: 3L (68C)
                                                     83; Conservative
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nes 77; Conserva
         Best Local Similarity
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R,Hauser, F.; Hoffmann, W.
J. Biol. Chem. 267, 24620-24624, 1992
A;Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.1
A;Reference number: A45155; MUID:93077556; PMID:1447205
1564 PPPTTTTTPPPPTTTTPSPPTTTTTPPPPTTTTPSPPTTTTPPPTTTPPPTTT
                                                                                                                 1624 TPI--TPPTSTTTLPPT----TTPSPPTTTTTPPPTTTPSPPTTTTPSPPTTTTP 1675
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                                                           99 FEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKB 158
                                                                                                                                                                         159 VPTTKPTEEPTINTTKTNITTTLLINNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSE 218
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C;Accession: A45155
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F; 307-347 Domain: trefoil homology (TRP3)
F; 556-66 Domain: trefoil homology (TRP4)
F; 551-613 Domain: trefoil homology (TRP5)
F; 621-661 Domain: trefoil homology (TRP6)
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APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Rang, Ajun
APPLICANT: Panger, Jouathan D.
APPLICANT: Panger, Gary R.
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APPLICANT: Carter, Darrick
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milns, Todd
APPLICANT: No. US20020128250Alman, Th
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US-10-025-380-1068
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APPLICANT:
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; Patent No. US20020110547A1
; GENERAL INFORMATION:
    APPLICANT: Wang, Aijun
    APPLICANT: Clapper, John A.
    APPLICANT: Maddleine J.
    APPLICANT: Maddleine J.
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    APPLICANT: Maddl
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                                                                                   1564 PPPTTTTTPPPPTTTTPSPPTTTTTPPPTTTTPSPTTTTPPPTTTTPPPTTTPSPFTT 1623
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         -- QTQPSKPTTKQRQNKPPNKPNNDFH 98
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                                                                                                                                                                                99 FEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKB
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15.7%; Score 193; DB 10; Length 5179;
Best Local Similarity 30.6%; Pred. No. 1.6e-06;
Matches 77; Conservative 23; Mismatches 114; Indels 38
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Publication No. US20020182191A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
56 ----VKSNLQPTTVKTKNTTTT
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US-09-833-263-1068
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US-10-025-380-1068
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272. 114
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
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APPLICATION NUMBER: US 07/390,901
              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                     Length 1367;
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Sequence 14, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                               ; Score 169.5; DB 10; Length
; Pred. No. 2.7e-05;
36; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
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APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/643,502
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FILING DATE: 08-AUG-1989
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
LENGTH: 1367
                                                                                                                                            ORGANISM: Saccharomyces cerevisiae
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COUNTRY: U.S.A.
                                                                                                                                                                                             Query Match
Best Local Similarity 26.2%;
Matches 62; Conservative 3
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                      Query Match
13.2%; Score 162; DB 14; Length 941;
Best Local Similarity 24.6%; Pred. No. 7e-05;
Matches 68; Conservative 26; Mismatches 104; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jacobs, Kenneth
Hewlick, Rochiey M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: 8T CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
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TELEPHONE: (617)876-1170
TELEPAX: (617)876-1170
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPEs: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
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FILING DATE: 29-DEC-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 84, Application US/10124557; Publication No. US20020137894A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----APTTKEP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TKKPTFKTTK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 KDL-----KPQTIKPKEVPTTKP-----TEBPTINTIKINITTLINNITGNPKLIS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 APITIKSAPITIPKEPAPITIPKKPAPITIPKEPAPITIPKEPITIPKEPAPITKEPAPITIPK 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 TTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV 65
                                                                                                                                                                                                                                                                                                                                                                                                                    78; Gaps
                                                                                                                                                                                                                                                                                                                                                                  Query Match
13.2%; Score 162; DB 14; Length 1022;
Best Local Similarity 24.6%; Pred. No. 7.8e-05;
Matches 68; Conservative 26; Mismatches 104; Indels 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 74, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gennet, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 KSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 NPTCWAICKRIPN-----KKPGKKTTTKP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                   NAME: CSETT, LUADIN
REGISTRATION NUMBER: 31,822
REGISTRATION INFORMER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-124-557-84
FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   LENGTH: 1022 amino acids
                                                                                                                                               TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                       TYPE: amino acid
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US-10-124-557-74
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66 K-----TKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 KDL-----KPQTTKPKEVPTTKP-----TEEPTINTTKTNITTLLINNTTGNPKLTS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1038;
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Genence 58, Application US/10124557

GENERAL INFORMATION:

APPLICANT: Turner, Katherine

Clark, Stephen C.

Jacobs, Renneth

Hewick, Rodney M.

Gener, Thomas G.

TITLE OF INVENTION:

Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
13.2%; Score 162; DB 14;
Best Local Similarity 24.6%; Pred. No. 7.9e-05;
Matches 68; Conservative 26; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 OMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
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                   FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CBETE, LUARN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (617)876-1170
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                    ;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-10-124-557-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1038 amino acids
                                                                                                                                                                                                                                                                                       TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
STATE: Massachusetts
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ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
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Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine;
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 K------TKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 TTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 104, Application US/10124557

Publication No. US20020137894A1

GENERAL INFORMATION:

APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Genner, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

COUNTER: 87 CambridgePark Drive
CITY: CambridgePark Drive
CITY: CambridgeFark Drive
COUNTEY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 1049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.2%; Score 162; DB 14; Length 10 Best Local Similarity 24.6%; Pred. No. 8e-05; Matches 68; Conservative 26; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
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                                                                                  FILING DATE: 18-7AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CREAT, LUATH
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
FILING DATE: 16-Apr-2002
PRIOR SASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-124-557-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617)876-1170
TELEPRA: (617)876-5851
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1049 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-124-557-104
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372 KSAPITPKEPAPITIKSAPITIPKEPAPITIKEPAPITIKEP------APITIKEP 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 NPTCWAICKRIPN-----KKPGKKTTTKP-------TKKPTFKTTK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 APTTTKSAPTTEKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 KDL-----KPQTTKPKEVPTTKP-----TEEPTINTTKTNITTTLLTNNTTGNPKLTS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 BPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 TTAILQDATSQIKWTTPTYLTQDPQLGISFSNLSRITSQTTTILASTTPGVKSNLQPTTV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 13.2%; Score 162; DB 14; Length 1140; Local Similarity 24.6%; Pred. No. 8.9e-05; hes 68; Conservative 26; Mismatches 104; Indels 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 TIKSAPITPKE ---PSPITIKEPAPITPKEPAPIT 572
                                                                                                     PRIOR DATE: 16-Apr-2002
CLASSIFICATION FUNDER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: -CURKNOWN-
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 39-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFRENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-51170
TELEFAX: (617)876-5851
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190 TSKVLAKPTPKAETTTK-----GPALTTPKEPTPTTPKEPASTTP---KEPTPTT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 K-----TKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TKKPTFKTTK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 APTTTKSAPTTPKEPAPTTPKKPAPTTPKBPAPTTPKEPTPTPKEPAPTTKEPAPTTPK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 KDL-----KPQTTKPKEVPTTKP-----TEBPTINTTKTNITTLLTUNTTGNPKLTS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 TTALIODATSQIKNTTPTYLTQDPQLGISFSNLSELTSQTTTLLASTTPGVKSNLQPTTV
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13.2%; Score 162; DB 14; Length 1270;
Best Local Similarity 24.6%; Pred. No. 0.0001;
Matches 68; Conservative 26; Mismatches 104; Indels 78
                                                                                                                                                                                                                                COMPUTER: INDEPT COMPUTER: FLOURY MILES
COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT 
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Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-124-557-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR
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66 K------TKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFBVFNFVPCSICSN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 АРТІТКЅАРТІРКЕРАРІТРККРАРІТРКЕРАРІТРКЕРТРІТРКЕРАРІТКЕРАРІТРК 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 KDL-----KPQTTKPKEVPTTKP-----TEEPTINTTKTNITTLLINNTTGNPKLTS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 BPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 KSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEP------APTTTKEP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 TTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%; Score 162; DB 14; Length 1311; 24.6%; Pred. No. 0.00011; tive 26; Mismatches 104; Indels 78
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
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                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: U8/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»

PRIOR APPLICATION: «Unknown»

PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
PILING DATE: 29-JUN-1990
PILING DATE: 29-DEC-1899
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1899
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1989
                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
    TOPOLOGY: linear
;    MOLECULE TYPE: protein
;    SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-124-557-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 142, Application US/10124557 Publication No. US20020137894A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1311 amino acids
                                                                                                                                                                             ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617)876-5851
                                                                                                    CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS
NUMBER OF SEQUENCES: 143
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nes 68; Conservative
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US-10-124-557-142
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US-10-124-557-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------APTTTKEP 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 APITIKSAPITPKEPAPITPKKPAPITPKEPAPITPKEPIPTTPKEPAPITKEPAPITPK 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 KDL-----KPQTTKPKEVPTTKP-----TEEPTINTTKTNITTTLLINNTTGNPKLTS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 TTALIQDATSQIKWTTPTYLTQDPQLGISFSNLSELTSQTTTLLASTTPGVKSNLQPTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
13.2%; Score 162; DB 14; Length 1313;
Best Local Similarity 24.6%; Pred. No. 0.00011;
Matches 68; Conservative 26; Mismatches 104; Indels 78
                                                                  INVENTION: Megakaryocyte Stimulating Factors SEQUENCES: 143
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 KSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 NPTCWAICKRIPN-----KKPGKKTTTKP----
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-DAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                         ADDRESSEE: Genetice Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5190
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1313 amino acids
TYPE: amino acid
Stephen C.
             Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               STATE: Massachusetts
                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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RESULT

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282 KSAPITPKEPAPITIFKEPAPITIFKEPAPITIFKEPAPITIFKEP 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 K------TKNTTTTQTQPSKPTTKQRQNKPNKPNNDFHFEVFNFVPCSICSN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 BPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 TTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV
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                                                                                                                 Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%; Score 162; DB 14; Length 1 24.6%; Pred. No. 0.00011; ive 26; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/124,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 NPTCWAICKRIPN-----KKPGKKTTTKP-
                                                                                                                                                                                                                                                                 ADDRESSER: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
'STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-124-557-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
Sequence 50, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1314 amino acids
                                                                      APPLICANT: Turner, Katherine Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617)876 - 5851
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 143
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SEQUENCE CHARACTERISTICS
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Best Local Similarity 24.6
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
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--TEEPTINTTKTNITTLLINNTTGNPKLTS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 K------TKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 TTALIQDATSQIKNTTPTYLIQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV 65
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                                                                                                                                                                                                                                 US-10-124-557-60

Sequence 60, Application US/10124557

Publication No. US20020137894A1

GENERAL INFORMATION:

APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:

SERET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.2%; Score 162; DB 14; Length 1320;
24.6%; Pred. No. 0.00011;
.ive 26; Mismatches 104; Indels 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                              457 TTKSAPTTPKE----PSPTTTKEPAPTTPKEPAPTT 488
                                                                                                     195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNV-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORIEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN RELEASE #1.0,
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-124-557-60
            147 KDL-----KPQTTKPKEVPTTKP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 60
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 24.68:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READMEILE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
APELICATION NUMBER: US/10/124,557
FILING DATE: I6-Apr-2002
CLASSIFICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APTICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                       RESULT 14
US-10-124-557-46

Sequence 46, Application US/10124557

Publication No. US20020137894A1

GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacoba, Kenneth
Hewick, Rodney M.
Gener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 KSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEP
451 TTKSAPTTPKE----PSPTTTKEPAPTTPKEPAPTT 482
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                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617)876-1170
TELEPAR: (617)876-5851
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Matches
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195 QWETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
457 TTKSAPTTPKE---PSPTTTKEPAPTTPKEPAPTT 488
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Search completed: October 29, 2003, 17:54:27 Job time : 41.7094 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 29, 2003, 17:36:05; Search time 12.6943 Seconds (without alignments) 773.267 Million cell updates/sec Run on:

US-09-462-816-4

1229 1 HKVTLTTAIIQDATSQIKNT.....VSTTSEHPSQPSSPPNTTRQ 232 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

328717 segs, 42310858 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:* Database :

1: /cgn2 6/prodata/2/laa/5A COMB.pep:*
2: /cgn2 6/prodata/2/laa/5B COMB.pep:*
3: /cgn2 6/prodata/2/laa/6A COMB.pep:*
4: /cgn2 6/prodata/2/laa/6B COMB.pep:*
5: /cgn2 6/prodata/2/laa/PCTUS COMB.pep:*
6: /cgn2 6/prodata/2/laa/PCTUS COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 8, Appli	Sequence 8, Appli	w	Sequence 8, Appli	w	w	Sequence 8, Appli		Sequence 12, Appl	œ	œ	œ	'n	'n	'n	Sequence 6, Appli	ø	27	4	Sequence 15, Appl	20	20,	Ξ,	તં	4,	Sequence 84, Appl	74,
	αI	US-08-467-963C-8	US-08-838-189D-8	US-08-852-344D-8	US-08-344-639E-8	US-08-467-969A-8	US-08-467-961A-8	US-08-001-554A-8	5194595-19	US-08-793-792-12	US-08-793-792-8	US-08-928-361B-8	US-09-588-995A-8	US-08-928-361B-5	US-09-588-995A-5	US-08-700-651-5	US-08-928-361B-6	US-09-588-995A-6	US-08-928-361B-27	US-08-793-792-4	US-08-700-651-15	US-08-928-361B-20	US-09-588-995A-20	PCT-US91-08177-13	US-08-276-967-2	US-07-757-022B-14	US-07-757-022B-84	US-07-757-022B-74
	DB	~	~	ო -	m _	۳ -	m 	m	9	e -	m	m	4	۳ -	4	т С	m	4	<u>س</u>	۳ ۳	e •	9	4	2	2	4	4	4
	Length	298	298	298	298	296	296	298	681	37	32	216	216	1837	1837	1721	1721	1721	216	28	249	245	243	263	247	941	1022	1038
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	73.3	18.1	15.7	15.3	15.3	15.3	15.3	15.3	15.3	15.3	14.8	14.2	14.1	14.1	14.1	13.9	13.4	13.2	13.2	13.2
	Score	1229	1229	1229	1229	1229	1229	1229	901	222	193	188	188	188	188	187.5	187.5	187.5	181.5	174	173.5	173.5	173.5	170.5	164.5	162	162	162
	Result No.	н	7	m	4	S	y	7	80	6	10	11	12	13	14	15	16	17	18	119	20	21	22	23	24	25	26	27

80144104064408 440406060444011	Sequence 17, Appl
US-07-757-022B-58 US-07-757-022B-104 US-07-757-022B-44 US-07-757-022B-44 US-07-757-022B-46 US-07-757-022B-60 US-07-757-022B-66 US-07-757-022B-66 US-07-757-022B-66 US-07-757-022B-66 US-07-757-022B-69 US-07-757-022B-2 US-07-757-022B-2 US-07-757-022B-2 US-07-757-022B-2 US-07-757-022B-2 US-07-757-022B-2 US-07-757-022B-2 US-07-757-022B-2 US-07-757-022B-2 US-08-706-518-34 US-09-216-393B-344 US-09-216-393B-344 US-09-216-393B-344 US-09-216-393B-344	US-09-588-995A-17
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162 162 162 162 162 162 162 162 162 163 163 163 163 163 163 163 163 163 163	158
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ALIGNMENTS

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APPLICANT: Michel H
APPLICANT: Michel H
APPLICANT: Michel H
APPLICANT: DU, Nun-Pan
APPLICANT: DU, Nun-Pan
APPLICANT: DU, Nun-Pan
APPLICANT: DU, Nun-Pan
APPLICANT: DU, Nun-Pan
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSE: Sim & McBurney
STREET: Gth Ploor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,189
FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-ANN-1993
PRICR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
RILING DATE: 06-ANN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-474 MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               ; Sequence B, Application US/08467963C; Patent No. 5968776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION POR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-467-963C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                     Canada
                                                                                                                                                                                                                                                                                                                                                        CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: M5G 1R7
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US-08-467-963C-8
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Gaps

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67 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 126
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Patent No. 6017539
GENERAL INFORMATION:
APPLICANT: EMASYSHYN, Mary E
TILLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBURNEY
STERET: GLAP FLOOF, 330 University Avenue
                                                                                                                                                                                                                                                                                                       LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
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Best Local Similarity 100.0%; Pred. No. 3e-105;
Matches 232; Conservative 0; Mismatches 0; Indels 0
      Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,344D
FILING DATE: US/08/852,344D
FILING DATE: US/08/852,344D
FILING APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION NUMBER: GB 9200117.1
FILING DATE: 05-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/POCKET NUMBER: 1038-688 MIS:jb
TELECOMMUNICATION INFORMATION:
      ;
0
    Mismatches
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COUNTRY: Canada
ZIP: MSG IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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  232; Conservative
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; TOPOLOGY: linear
US-08-852-344D-8
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                                                                                                                                      67 HKVILITAIIQDATSQIKNITPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 126
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APPLICANT: EMASYBLYN, Mary B
APPLICANT: DV, Run-Pan
APPLICANT: EMASYBLYN, Mary B
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
CORRESPONDENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & McBurney
                                                            Gaps
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           Score 1229; DB 2; Length 298; Pred. No. 3e-105; 0; Mismatches 0; Indels 0
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                                                                                                1 HKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSELTSQTTTI
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,189D
CLASSIFICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
CLASSIFICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 1038-687 MIS:jb
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: RIGHT SECOND INC. 8:
SEQUENCE CHARACTERISTICS:
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6th Floor, 330 University Avenue
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5998169
GENERAL INFORMATION:
           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 232; Conservative 0
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COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
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121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: ISM PC compatible COMPUTER: Eloppy disk COMPUTER: IBM PC compatible OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,969A FILING DATE: 06-JUN-1995 CLASSIFICATION NUMBER: US 08/001,554 FILING DATE: 06-JUN-1993 CLASSIFICATION: 435 PRIOR APPLICATION: 435 PRIOR APPLICATION NUMBER: GB 9200117.1 FILING DATE: 06-JAN-1992 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION
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100.0%; Pred. No. 3e-105;
iive 0; Mismatches 0;
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STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08467969A
Patent No. 6168786
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Ewasyshyn, Mary E
ITILE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH 2.98 amino acids
TYPE: amino acids
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 100.0
Matches 232; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bingle
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COUNTRY: Canada
ZIP: MSG 1R7
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STATE: Ontario
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QPITVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
                                                                                                                                  QPITVKIKNITITQTQPSKPTIKQRQNKPPNKPNNDFHFEVPRVPCSICSNNPICMAIC 186
                                                                                                                                                                                                                  KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 180
                                                                                                                                                                                                                                                        187 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 246
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APPLICANT: Ewasyshyn, Mary E
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFUENZA VIRUS
TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
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ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08344639E
Patent No. 6033668
GENERAL INFORMATION:
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REGISTRATION NUMBER: 24,973
REFERENCE/POCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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US-08-344-639E-8
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67 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 126
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STREET: 330 University Avenue, 6th Floor
SITY: Toronto
SIATE: Ontario
COUNTRY: Canada
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08001554A
Patent No. 6225091
GENERAL INFORMATION:
APPLICANT: Riein, Michel H
APPLICANT: Riein, Michel H
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIPICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/POCKET NUMBER: 1038-286
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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06-JAN-1993
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TELBERX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE:
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ONTINKTANTITYOTOPSKPITKORONKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
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                                                                                                                                                                             187 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTBEPTINTTKTNITTT
                                                                QPITVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC
                                                                                                                                            KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,961A
FILING DATE: 06-JUN 1995
RIOR APPLICATION TO BATA:
APPLICATION NUMBER: US/08/001,554
FILING DATE: 06-JUN-1993
CLASSIFICATION ATA:
APPLICATION NUMBER: 06-JUN-1993
CLASSIFICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
RESTSTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION NUMBER: 1038-476 MIS:bh
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100.0%; Score 1229; DB 3;
Best Local Similarity 100.0%; Pred. No. 3e-105;
Matches 232; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 University Avenue, 6TH Floor
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
AITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
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MOLECULE TYPE: DNA (genomic)
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M5G 1R7
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CITY: Toronto
STATE: Ontario
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127 QPITVKIKNITITQCQPSKPTTKQRQNKPPNKPNNDFHFBVFNFVPCSICSNNPTCWAIC
                                                             KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTEEPTINTTKTNITTT
                                                                                                    187 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT
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                                                                                                                                                                                                         247 LLTNNTTGNPKLTSQMETFHSTSSBGNLSPSQVSTTSEHPSQPSSPPNTTRQ 298
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,554A
FILING DATE: 06-JAN-1993
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US-08-793-792-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                      RESULT 10
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TITLE OF INVENTION: Antigenic peptides derived from the
TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
NUMBER OF SEQUENCES: 13
COMPUTER READLE FORM:
MEDIUM TYPE: LOPOPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  610 KPQTTKSKEVPTTKPTEEPTINTTKTNIITTLISNTTGNPELISQMETFHSTSSEGNPS 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 QLGISPSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                      247 LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 298
181 LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 73.3%; Score 901; DB 6; Length 681; Best Local Similarity 91.0%; Pred. No. 1.2e-74; Matches 172; Conservative 6; Mismatches 11; Indels
                                                                                                                                                             APPLICANT: WATHEN, MICHAEL W.
TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING
,IMMUNOSENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                   ; INDUCTION OF SECURICES: 19
; VUMBER OF SECURICES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,780
; FILING DATE: 31-0CT-1988
; PRIOR APPLICATION NUMBER: 137,387
; FILING DATE: 23-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                             5194595
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                                                                                                                       5194595~19
;Patent No.
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Antigenic peptides derived from the G-protein of RSV for type- and subtype-specific diagnosis of respiratory syncytial virus (RSV) infection.
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TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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                                                        Gaps
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Query Match
18.1%; Score 222; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.3e-14;
Matches 37; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.7%; Score 193; DB 3; Length 32; 100.0%; Pred. No. 2.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                   91 NKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 127
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APPLICATION NUMBER: US/08/928,361B
                                                                                                                            1 NKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 37
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tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: PETERS, VERNY, JONES & BIKSA: 385 Sherman Avenue, Suite 6
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 8, Application US/08928361B; Patent No. 6071518
                                                                                                                                                                                                                                                         ; Sequence 8, Application US/08793792; Patent No. 6077511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Conservative
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Anti-
TITLE OF INVENTION: G-px
TITLE OF INVENTION: Of x
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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ZIP: 94306-1840
COMPUTER READABLE FORM:
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STRANDEDNESS: sin
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650-324-1678
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
Query Match
Best Local Similarity
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US-08-928-361B-5
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| GENERAL INFORMATION: | APPLICANT: BERNAISE |
| APPLICANT: BERNES, DEBRA A. |
| APPLICANT: BRENES, DEBRA A. |
| APPLICANT: BRENES, DEBRA A. |
| APPLICANT: BRENES, DEBRA A. |
| APPLICANT: GTT, JIRI
| TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM |
| TITLE OF INVENTION: INFECTIONS |
| FILE REFERENCE: 480.19-5 |
| CURRENT APPLICATION NUMBER: 08/92, 361 |
| PRIOR APPLICATION NUMBER: 08/92, 361 |
| PRIOR FILING DATE: 1997-09-12 |
| PRIOR APPLICATION NUMBER: 08/700, 651 |
| PRIOR FILING DATE: 1995-04-03 |
| PRIOR FILING DATE: 1995-04-03 |
| NUMBER: OF SEQ ID NOS: 115 |
| SEQ ID NO S: 115 |
| LENGTH RESERVED |
| LENGTH RESERVED |
| LENGTH RESERVED |
| LENGTH RESERVED |
| SEQ ID NO S: 115 |
| LENGTH RESERVED |
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15.3%; Score 188; DB 3; Length 216;
Best Local Similarity 26.4%; Pred. No. 8.3e-10;
Matches 60; Conservative 23; Mismatches 120; Indels 24; Gaps
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                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1 (HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
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Patent No. 6514697
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; ORGANISM: Cryptosporidium parvum
US-09-588-995A-8
                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 8:
12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS:
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MOLECULE TYPE: protein
                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-588-995A-8
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Sequence 5, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INPECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                64 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 123
                                                                                                                                                                                                                                                                                      124 PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTLLT 183
                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                         Gaps
                                                                                                                   4 TLITALIQDATSQIKNTIPTYLIQDPQLGISFSNLSEITSQITTILASTIPGVKSNLQPT
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Best Local Similarity 26.4%; Pred. No. 1.4e-08;
Matches 60; Conservative 23; Mismatches 120; Indels 24;
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   Length 216;
ch 15.3%; Score 188; DB 4; Length 216 I Similarity 26.4%; Pred. No. 8.3e-10; 60; Conservative 23; Mismatches 120; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEB: PETERS, VERNY, JONES & BIKSA
F: 385 Sherman Avenue, Suite 6
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
ATYONREV/ASERT US 60/026,062
ATYONREV/ASERT US 60/026,062
ATYONREV/ASERT US 60/026,062
ATYONREV/ASERT US 60/026,062
ATYONEV/ASERT US 60/026,062
ATYONER/ASERT US 60/026,062
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 5:
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APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DERAA A.

APPLICANT: BARNES, BERAA A.

APPLICANT: BARNES, RICHARD C.

APPLICANT: NELSON, RICHARD C.

TITLE OF INVENTION: INCIDENCE FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INSCIATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

FILE REFERENCE: 480.19-5

CURRENT APPLICATION NUMBER: 08/928, 361

PRIOR APPLICATION NUMBER: 08/700,651

PRIOR FILING DATE: 1997-09-12

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 115

SEQ ID NO SEQ ID NOS: 115

SEQ ID NO SECOTION OF SEQ ID NOS: 118-15
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                                                                                                                                                                                                                                 Sequence 5, Application US/08700651B
PATENT NO. 60158B2
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09588995A
Patent No. 6514697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Cryptosporidium parvum
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Best Local Similarity 26.48
Matches 60; Conservative
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US-09-588-995A-5
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US-08-700-651-5
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APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: PREPAIRED OF CRYPCOSPORTIGIUM PARVUM
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPCOSPORTIGIUM PARVUM
TITLE OF INVENTION: INFECTION
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
EARLIER PILING DATE: 1997-08-14
EARLIER PILING DATE: 1995-04-03
RUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO S: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 OPTIVKTKUNTITIQIOPSKPITKORQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.3%; Score 187.5; DB 3; Length 1721; 25.6%; Pred. No. 1.4e-08; tive 21; Mismatches 125; Indels 31;
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Matches 61, Conservative
APPLICANT: LEECH, JAMES
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Respiratory syncit Membrane bound g p Sequence of human HSRV glycoprotein Respiratory syncyt Chimeric human res RSV G protein pept
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.: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1980.
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
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AAR39286
AAW96313
AAR70845
AAR25302
AAW47605
AAU74676
AAP90441
ABP97862
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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572.5 564.5 564.5 564.5 558 558 558 558 558 558 558 558 558 5	66 44 44 44 44 44 44 44 44 44 44 44 44 4		100 100 100 100 100 100 100 100 100 100	of r tory spons acti ial v CAC S-089 LAB I
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                                                                                                         vector. The G protein gene into a non-replicating vector. The G protein gene into a non-replicating vector. The G protein is placed under the control of alternative signal and expression sequences, for example the chimeric G protein produced may also comprise the signal peptide of tissue plasminogen activator (tPA). The recombinant vector may also comprise sequences immunoprotective ability. The resulting immunogenic composition will generate antibodies directed against the RSV G protein when administered to a host organism. The composition is useful as a continuise against RSV-associated disease, particularly resulting in a balanced Th/Thz immune response and for raising Ab, by usual immunisation and cell fusion methods. This truncated G protein is secreted since it lacks a transmembrane domain.
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                                                                                                                                                                                                                                                                                                                                                                                               Gaps
containing the protein G sequence, useful in protective vaccines and to raise antibodies for diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
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                                                                                                 syncytial virus (RSV) G protein can be
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                                                                                                                                                                                                                                                                                                                                                             Score 1229; DB 20
Pred. No. 3.6e-89;
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                                                                   Claim 9; Fig 3; 67pp; English
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(first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  232 AA;
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13-JAN-1994
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A novel multimeric hybrid gene is used as a vaccine. The gene consists of two gene sequences which are linked and encode antigenic regions, these two sequences being derived from two different pathogens (parainfluenza virus (PIV) and respiratory syncitial virus (RsV)). The gene sequences that are particularly used are those which encode PIV-3 F and HN proteins (AAQ45683, AAQ45684) and RSV F and (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic composition for generating antibodies against respiratory syncytial virus - comprises non-replicating vector containing the protein G sequence, useful in protective vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein; respiratory syncytial virus; RSV; recombinant vector; vaccine; immune response; immunogenicity; tPA; antibody; tissue plasminogen activator.
                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                              DB 14; Length 298;
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                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Membrane bound G protein of respiratory syncytial virus.
           Multimeric hybrid genes and their chimeric proteins vaccines against multiple pathogenic infections e.g. para-influenza virus and respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                          100.0%; Score 1229; DB 14
100.0%; Pred. No. 4.7e-89;
tive 0; Mismatches 0;
                                                                               Claim 11; Figure 7A-7D; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                            Matches 232; Conservative
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                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                             298 AA;
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                                                                                                                                                                                                                                                                                                       67 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 126
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                                         The respiratory syncytial virus (RSV) G protein can be used in vaccines by inserting the G protein gene into a non-replicating vector. The G protein is placed under the control of alternative signal and expression sequences, for example the chimeric G protein produced may also comprise the signal peptide of tissue plasminogen activator (tPA). The recombinant vector may also comprise sequences immunoprotective ability. The resulting immunogenic composition will agenerate antibodies directed against the RSV G protein when administered to a host organism. The composition is useful as a vaccine to immunise against RSV-associated disease, particularly, by usual immunisation and cell fusion methods.
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                  100.0%; Score 1229; DB 20; Length 298; 100.0%; Pred. No. 4.7e-89; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of human respiratory syncytial virus (HRSV) A2 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human respiratory syncytial virus (HRSV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP70845 standard; protein; 298 AA
to raise antibodies for diagnosis
                      Claim 4; Fig 2; 67pp; English.
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(first entry)
                                                                                                                                                                                                                                                        Matches 232; Conservative
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                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                             298 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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61 QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFBVFNFVPCSICSNNPTCWAIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HKVTLTTAIIQDATSQIKNTTFTYLTQDPQLGISPSNLSEITSQTTTILASTTPGVKSNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 LLTSNTTGNPELTSQMETFHSTSSEGNPSPSQVSTTSBYPSQPSSPRNTPRQ 298
                                                                                                               A novel plasmid which comprises a DNA sequence encoding this protein, and the protein itself, are claimed, for use as HRSV vaccines. The vaccine can be administered to pregnant women or women of child bearing age to stimulate maternal antibodies. Infants can also be vaccinated at 2-3 months of age. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                         91.1%; Score 1120; DB 8; Length 298; 92.7%; Pred. No. 1.8e-80; tive 5; Mismatches 12; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccines for human respiratory virus - include structural greading for native structural viral proteins and immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human respiratory syncytial virus strain A2
                                                         Disclosure; Chart 13; 57pp; English.
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88US-0218737.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 92.7 Matches 215; Conservative
syncytial virus proteins.
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                                                                                                                                                                                                                                                                                                                                   298 AA;
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                                                                                                                                                                                                                                                                                                                                   Sequence
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vaccines against HRSV.

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AAQ29622-26. The proteins are F, G, 22K, 9.5K and major capsid protein N. The sequences and encoded proteins are useful for preparing vaccines against HRSV. The vaccines can be used to confer immunity against respiratory tract infections on human subjects. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Production of human respiratory syncytial virus glyco-protein F or (-by culturing eukaryotic host cells transfected with corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence was used in the development of a novel method for the production of human respiratory syncytial virus (HRSV) glycoprotein G (595). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV 9PF or 9PG. The 9p can be used to prepare
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                                                                                                                                                                                                                                                                                                                                                          LLTINITTGNPKLISQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ
                                                                                                                      91.1%; Score 1120; DB 13; Length 298; 92.7%; Pred. No. 1.8e-80; ive 5; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine.
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86US-0818740.
86WO-US02756.
92US-0897171.
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                                                                                                                       Query Match
Best Local Similarity
                                                                                          298 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the inventors transcer or excompanies. Compared to the state of the antigenic fragment. The virus may be administered in combination with an antivixal chemotherapeutic compound. Two or more viruses expressing different PWV proteins may be co-administered. Compositions comprising the virus are useful for eliciting a humoral and/or cellular immune response to a PMV in a mammal, particularly a human. Further a recombinant Sendai virus comprising an exogenous nucleic acid
                                                                                     1 HKVTLITALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                                              KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEBPTINTTKTNITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSV; G protein; heavily glycosylated protein; antianaemic; antiviral; vaccine; gene therapy; paramyxovirus; sendai virus; PMV; antiviral chmotherapeutic compound; humoral response; cellular immune response; hFVV; paediatric respiratory disease; globin gene transfer; sickle cell disease; beta-thalassaemia; human immunodeficiency virus infection; HIV.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Sendai virus useful in vaccines to protect infection by paramyxoviruses, comprises exogenous nucleic acid encoding paramyxovirus protein or its antigenic fragment
                                                                                                                                                                                                                                                                                       LLINNITIGNPKLISQMETFHSTSSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a recombinant Sendai virus comprising
                               298;
                               Length
                                                            Indels
                            Score 1120; DB 19;
Pred. No. 1.8e-80;
5; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syncytial virus G protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 48; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                              AAU74676 standard; Protein; 298
                          91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-2001; 2001WO-US16610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                         Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takimoto
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                                          Local Similarity
298 AA;
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Sequence
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                          Query Match
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encoding a second PMV protein is also administered and priming and/or boosting humoral or cellular immune response comprises administering one or more of a recombinant or isolated PMV protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendai viral vector encoding a PMV protein. The recombinant virus is useful as an effective vaccine against helv or SBV (the major causes of paediatric respiratory disease) and also to express any gene of interest in target cells, providing a positive medical impact on impaired cells, Mild-type globin gene transfer (i.e. gene therapy) into stem cells effects a cure for sickle cell disease or betathalssaemia. The recombinant virus may also prove effective in conferring immunity to human immunodeficiency virus (HIV) infection. The Sendai virus replicates at level that is high enough to induce sufficient immunity, but does not cause any harm to human recipient. The present esquence represents a respiratory syncytial virus (RSV) @ protein (heavily glycosylated protein), a PMV protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 HKVTPTTAIIQDATSQIKNTTPTYLTQNPQLGISPSNPSEITSQITTILASTTPGVKSTL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 KRIPNKKPGKKTTTKPTKKPTLKTTKKDPKPQTTKSKEVPTTKPTEEPTINTTKTNIITT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 QSTTVKTKNTTTTQTQPSKPTTKQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 LLTINNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 LLTSNTTGNPELTSQMETFHSTSSEGNPSPSQVSTTSEYPSQPSSPDNTPRQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric human respiratory synctial virus glycoproteins F and G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                           91.1%; Score 1120; DB 23; Length 298; 92.7%; Pred. No. 1.8e-80; ive 5; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric human respiratory syncytial virus polypeptides(s)
- contg. immunogenic fragments from HRSV glycoproteins
F and G, for vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric polypeptide; human respiratory syncytial virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP90441 standard; protein; 681 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein F; protein G; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88WO-US03784.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 92.7
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                       298 AA;
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                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP90441;
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                                                                                                                                                                                                                                                                                                                                      90 PNKPNNDFHPEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDL 149
                                                                                                                                                                                                                                                                                                                                                                        550 PSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTLKTTKCDP 609
                                                                                                                                                                                                                                                                                                                                                                                                            150 KPQTTKPKEVPTTKPTEEPTINTTKTNITTTLLTNNTTGNPKLTSQMETFHSTSSEGNLS 209
                                                                                                                                                                                                                                                                                                                                                                                                                               010 KPQTTKSKSVEVPTTKPTEEPTINTTKTNITTITLTSNTTGNPELTSQMETFHSTSSEGNPS 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a fusion protein comprising a peptide derived from the G protein of Respiratory syncytial virus (RSV) linked to a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide generates an immune response against any antigen coupled to it, and and has a negative, immediate hypersensitivity response. Diphtheria
                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                  30 QLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccines, lacks at least one Cys residue, also related nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide derived from diphtheria anatoxin, useful as carrier in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diphtheria anatoxin; immune response; antigen; carrier; G protein; hypersensitivity response; vaccine; infection; RSV; cancer.
                                               Chimeric polypeptide contg. a signal sequence and one or more mimulogenic fragments from both human respiratory syncytial virus glycoproteins F and G. Can be used in vaccines. Hosts are, eg E. coli, Chinese hamster ovary cells, murine C127 cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSV G protein peptide G2Na and diphtheria anatoxin peptide DTb.
                                                                                                                                                                                            Length 681;
                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                            73.3%; Score 901; DB 10; 91.0%; Pred. No. 8.6e-63; ive 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 27-28; 42pp; French.
                  Claim 3; page 47-48; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP97862 standard; protein; 361 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corvaia N, Nguyen NT, Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-2001; 2001FR-0009733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-2001; 2001FR-0009733.
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                                                                                                                                                                                                                              Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 PSQVSTTSE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    670 PSOVNISSO 678
                                                                                                                                                                                                             Similarity
                                                                                                                                                            681 AA;

 frugiperda.

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                                                                                                                                                            Sequence
                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                        64 PNKKPGKKTTTKPTKKPTKKTTKKDHKPQTTKPKEVPTTKP---GSINLDMDVIRDKTKT 120
                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a fusion protein comprising a Klebsiella pheumoniae outer membrane protein A (OmpA) designated P40 and a respiratory syncytial virus (R8V) antigen. Enterobacterium OmpA proteins, associated with an immunogenic peptide from R8V are used to prepare a nasal composition that induces a protective response, against R8V infection in the upper and lower (lung) respiratory tract. OmpA potentiates the immune response to some immunogenic peptides, eliminating the need for adjuvants. The method is useful for producing
anatoxin derived peptides, when modified to lack at least one cysteine residue, are useful as carrier peptides. Deletion of Cys residues in anatoxin peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal infections, or cancers and to generate, or increase, an immune response against infectious agents or tumour cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OmpA; P40; enterobacteria; nasal composition; respiratory tract; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine against respiratory syncytial virus, comprises enterobacterial outer membrane protein and viral immunogen, provides protective response throughout the respiratory tract
                                                                                                                                                                                                                                                                                  4 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI
                                                                                                                                                                                                                                                64 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a fusion protein of P40 and RSV antigen.
                                                                                                                                                                               Length 361;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                     176 NITT-----TLLIMNTTGNPKLTSQMETFHSTSSE 205
                                                                                                                                                                                                                                                                                                                                                                                                                      121 KIESLKEHGPIKNKMSESPNKTVSEEKAKQYLEEFHQTALE
                                                                                                                                                                                                                   50;
                                                                                                                                                                             Score 580; DB 24;
Pred, No. 8.3e-38;
                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 31-32; 39pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB67771 standard; Protein; 452
                                                                                                                                                                         47.2%;
70.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                           Local Similarity 70.8
nes 114; Conservative
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                                                                                                                                           361 AA;
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                                                                                                                                           Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            response
                                                                                                                                                     322 LAPDRRVBIEVKGYKEVVTQ-----PQGPG-----DPMTVKTKNTTTTQTQPSKPTTKQ
                                                                                                                                                                                     85 RONKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKPGKKTTTKPTKKPTFKT
                                                                                                                                                                                                       371 RQNKPPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide derived from diphtheria anatoxin, useful as carrier in vaccines, lacks at least one Cys residue, also related nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diphtheria anatoxin; immune response; antigen; carrier; G protein; hypersensitivity response; vaccine; infection; RSV; cancer.
                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSV G protein peptide G2Na and diphtheria anatoxin peptide DTa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infections, or cancers and to generate, or increase, an immune against infectious agents or tumour cells.
                                                                  Length 452;
                                                                                               Indels
                                                                                                                         25 LTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKNT
 vaccines for prevention or treatment of RSV infections
                                                                DB 22;
                                                                                             18;
                                                             Score 572.5; DB 2
Pred. No. 4.2e-37;
                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 26-27; 42pp; French.
                                                                                                                                                                                                                                                   145 TKKOLKPOTTKPKEVPTTKPTE 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                            ABP97861 standard; protein; 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beck A;
                                                               46.68;
76.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Respiratory syncytial virus.
Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-2001; 2001FR-0009733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-2001; 2001FR-0009733
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                            Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nguyen NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-241969/25
                                                                             Similarity
                              452 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FR2827606-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                           ABP97861;
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                               Local
                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                            ABP97861
SXS
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DB 24; Length 291;

45.9%; Score 564.5;

Query Match

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3;
                                                                                                                                                                                                                                                                                              64 PNKKPGKKTTTKPTKKPTFKTTKKDHKPQTTKPKSVPTTKPGSGADDVVDSSKSFV---- 119
                                                                                                          64 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derived from the optocein of Respiratory syncytial virus (RSV) linked to a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide generates an immune response against any antigen coupled to it, and and has a negative, immediate hypersensitivity response. Diphtheria anatoxin derived peptides, when modified to lack at least one cysteine residue, are useful as carrier peptides. Deletion of Cys residues in anatoxin peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal infectious, or cancers and to generate, or increase, an immune response against infectious agents or tumour cells.
                                                                                                                                                                                                                                                        124 PNKKPGKKTTTKPTRKPTFKTTKKDLKPQTTKPKBVPTTKPTE--BPTINTTKTNITTL 181
                                                                                                                                                                               63
                                                                                                                                                     4 TVKTKNYTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a fusion protein comprising a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide derived from diphtheria anatoxin, useful as carrier in vaccines, lacks at least one Cys residue, also related nucleic acids
                                  23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diphtheria anatoxin; immune response; antigen; carrier; G protein; hypersensitivity response; vaccine; infection; RSV; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSV G protein peptide G2Na and diphtheria anatoxin peptide DTaDTb
Pred. No. 1.1e-36;
10; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               182 LINNITIGNPKLISQMETFHSTSSEGNLSPSQVSTISEHPSQPSS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 29-30; 42pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP97863 standard; protein; 548 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corvaia N, Nguyen NT, Beck A;
67.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-2001; 2001FR-0009733,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-2001; 2001FR-0009733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                      Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-241969/25.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FR2827606-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP97863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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64 PNKKPGKKTTTKPTKKPTFKTTKKDHKPQTTKPKEVPTTKFGSGADDVVDSSKSFV--- 119
                                124 PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTE--EPTINTTKTNITTL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence comprises a 219 amino acid fragment of streptococcal protein G, designated BB, fused to an immunogen, designated G2A, derived from amino acids 130-230 of protein G from Respiratory Syncytial Virus sub-group A or B. The BB fragment is able to bind to human serum albumin and thereby enhance immunogenicity of any antigen, hapten or immunogen that is covalently coupled to it. In this specific example, the BB fragment was found to induce T helper memory cells, leading to production of anti-G2A antibodies by stimulated
4 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 63
                                                                                                                                                                                                                                                                                                                                 Streptococcus; protein G; carrier protein; immunogenicity; increase; enhance; vaccine; anti-viral; human serum albumin; binding; immunostimulation; respiratory syncytial virus; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enhancing immunogenicity by coupling immunogen to serum
albumin-binding protein - useful for preparing improved vaccines,
e.g. against Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 562; DB 17; Length 349; Pred. No. 2.1e-36;
                                                                                                                                                                                                                                                                                                      Streptococcal protein G fragment BB fused to RSV hapten G2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Binz H, Nguyen Ngoc T, Nygren PA, Stahl S;
                                                                                            182 LTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSS 225
                                                                                                                         120 -------MENF---SYHGTKPGYVDSIQKGIQKPKS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247..347
/label= G2A
/note= "residues 130-230 of RSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...23
|label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 81-83; 102pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric Streptococcus sp.
Chimeric Respiratory Syncytial Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                         AAR95660 standard; Protein; 349 AA.
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78.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94FR-0013310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-FR01466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24..242
/label= BB
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-251766/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT31647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-1995;
                                                                                                                                                                                                                                                                     21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9614416-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andreoni C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                       AAR95660;
                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uhlen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
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21; Indels 23; Gaps

DB 24; Length 548;

Ouery Match 45.9%; Score 564.5; DB 2. Best Local Similarity 67.1%; Pred. No. 2.2e-36; Matches 110; Conservative 10; Mismatches 21

64 TVKTKNTTTQTQPSKPTTKQRQNKPPNNDFHFEVFNFVPCSICSNNPTCWALCKRI 123

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                                                     272
                                                                             PNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDL 149
                                                                                                          332
                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a method which uses quaternary aliphatic ammonium salts together with an immunogen or antigen to treat syncytial virus infections. The combination of the salt with the antigen or immunogen improves immunogenicity and equilibrates the Thl/Th2 immune response. The method is used for the treatment of respiratory syncytial virus infections. The present sequence represents a fusion protein, comprising an albumin binding domain of the G protein of Streptococcus sp. fused to a G protein fragment of respiratory syncytial long version). The fusion protein is used as an antigen in the method
                                                                                                                                                                                                                                                                                                                                Aliphatic ammonium salt; immunogen; antigen; syncytial virus infection;
                                                                                                                                                                                                                                                                                                      Amino acid sequence of fusion protein comprising 2 G protein fragments.
                                                                                            37 NLSEITSQTTT--ILASTT-----PGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                         Use of quaternary aliphatic ammonium salt and immunogen or antigen to combat respiratory syncytial virus infections
  10; Gaps
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        120..230
/note= "G protein fragment of VRS"
 10;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                       AAB68028 standard; Protein; 349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FABR ) FABRE MEDICAMENT SA PIERRE.
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10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nguyen TN;
                                                                                                                                150 KPQTTKPKEVPTTKPTE 166
                                                                                                                                               333 KPQTTKPKEVPTTKPVD 349
                                                                                                                                                                                                                                                                                                                                                                                                 Respiratory syncytial virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99FR-0011284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99FR-0011284
                                                                                                                                                                                                                                                                                                                                              G protein; fusion protein.
                                                                                                                                                                                                                                                                             (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beck A, Klinguer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-267782/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAF84711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FR2798292-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-SEP-1999;
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                                                                                                                                                                                                                                                                              29-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-2001
Matches 107;
                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                             9
                                                                                                                                                                                                                                                    AAB68028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Protein
                                                                                                                                                                                              RESULT 14
AAB68028
ID AAB68
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The sequence of the wild type amino acid residues 130-230 from the protein G of the respiratory syncytial virus (RSV) subgroups A. The sequence was used to synthesise the immunogenic peptides AAR88245-52 based on residues 174-187 of the subgroup A and B RSVs. The peptides are pref. conjugated to a novel carrier protein (the p40 protein; see AAR88257) derived from a membrane lipopolysaccharide (LPS) fraction from Klebsiella membrane LPSs with a divalent cation and detergents. Ribsiella membrane LPSs with a divalent cation and detergents, obtain an immunological adjuvant and linking the p40 protein to the above peptides. The conjugates are useful in the treatment of RSV A or B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                    149
                  273 PNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKPGKKTTTKPTKKPTFKTTKKCH 332
                                                                                                                                                                                                                                                                                                                                                                     Immunogenic peptide; protein G; respiratory syncytial virus; adjuvant; carrier protein; membrane lipopolysaccharide; LPS; Klebsiella pneumoniae; divalent cation; detergent; anion-exchange chromatography; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFBVFNFVPCSICSNNPTCWAICKRI 123
      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
37 NLSEITSQTTT--ILASTT----PGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                             PNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New respiratory syncytial virus polypeptide(s) for vaccine prodn. esp. by conjugation with new Klebsiella pneumoniae p40 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Pred. No. 1e-36;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                       RSV subgroup A wild type residues 130-230 (G2A clone).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thien NN, Trudel
                                                                                                                                                                                                                                         AAR88253 standard; peptide; 101 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 23; 38pp; French.
                                                                                                                             KPQTTKPKEVPTTKPTE 166
                                                                                                                                                         333 KPOTTKPKEVPTTKPVD 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Respiratory syncytial virus.
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                                                                                                                                                                                                                                                                                                         (first entry)
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Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baussant T, Binz H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-353189/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2718452-A1
                                                                                                                                                                                                                                                                                                         15-MAY-1996
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                                                                                                                             150
                                                             90
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                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                          AAR88253
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124 PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKP 164

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Gaps

Query Match
45.7%; Score 562; DB 22; Length 349;
Best Local Similarity 78.1%; Pred. No. 2.1e-36;
Matches 107; Conservative 10; Mismatches 10; Indels 10;

q

Search completed: October 29, 2003, 17:38:01 Job time : 53.966 secs